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January 24, 2002, 09:08:13; Search time 23.82 Seconds (without alignments) 410.482 Million cell updates/sec
                                                                                                                                                                                     US-09-905-235-1
675
1 MCDAFVGTWKLVSSENFDDY......KLVVECVMKGVTSTRVYERA 132
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                              522463 segs, 74073290 residues
                                                                         using sw model
                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                         - protein search,
                                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                                                                                     Scoring table:
                                                                       OM protein
                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                              Searched:
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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

| SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
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/SIDS8/gcgdata/geneseg/genesegp/AA2001.DAT:* /SIDS8/gcgdata/geneseg/genesegp/AA1999. /SIDS8/gcgdata/geneseg/genesegp/AA2000. /SIDS8/gcgdata/geneseg/genesegp/AA1998 /SIDS8/gcgdata/geneseg/genesegp/AA199

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Š

Description	Human AFABP protei	Mouse AFABP prote1	Mouse MDGI polypep	Human myelin P2 pr	MDGI active peptid	Human MDGI polypep	Bovine MDGI polype	Bovine myelin P2 p	Porcine heart-fatt	Human cytostatin I	Amino acid sequenc
QI	AAY90320	AAY90319	AAG66576	AAW4 0227	AAR13559	AAG66578	AAG66577	AAW40228	AAW31534	AAW22408	AAW80949
. DB	21	21	22	19	12	22	22	19	18	18	19
Query Match Length DB	132	132	133	136	131	. 133	133	136	134	132	132
Query Match	100.0	95.6	69.0	67.9	67.1	66.5	66.1	62.9	64.5	59.1	59.1
Score	675	625	466	458	453	449	446	445	435.5	399	399

Reducing expression of adipocyte fatty acid binding protein through administration of a compound is used to inhibit formation of an atherosclerotic lesion -

Human cytostatin I		Human secreted pro	**	Human secreted pro		Breast and ovarian		Human colon cancer	Human 5' EST relat		Schistosoma manson	CRABP-I gene produ	Human secreted pro	CRABP-II gene prod	Human lung tumour	Lung cancer associ	Human secreted pro	Human cancer assoc	Human polypeptide	Human cellular ret	Human polypeptide	Human cytostatin I	Human cytostatin I	Human cytostatin I	Retinol-binding pr	Human retinoid bin	Retinol-binding pr	⊏	Human cytostatin I	Human cytostatin I	Human growth inhib	Human cytostatin I	. Human cellular ret
AAW81106	AAW82403	AAG03847	AAG66580	AAG03957	AAR75423	AAB58740	AAR55866	AAG75123	AAY65303	AAW68550	AAR75643	AAR42212	AAG01405	AAR42211	AAB76852	AAB58158	AAG01603	AAB43403	AAM38758	AAB60659	AAM40544	AAW30891	AAY32504	AAG66575	AAU02203	AAY92910	AAU02202	AAW27561	AAW26581	AAY49535		AAG66579	AAP82557
19	50	21	22	21	16	21	15	22	21	20	16	14	21	14	22	21	21	21	22	22	22	18	20	22	22	21	22	18	18	20	20	22	6
132	132	117	131	132	132	88	135	82	69	134	$^{\circ}$	137	26	138	138	149	66	160	135	135	168	135	135	135	135	135	156	101	107	107	107	106	52
59.1	59.1	æ	57.3	9.95	56.4	55.6	54.2	53.3	40.0	35.1	34.0	32.9	Ξ.	g	29.9	29.9	28.7	27.6	24.4	24.4	24.4	24.3	24.3	24.3	24.3	24.0	20.1	18.1	18.1	18.1	18.1	17.1	16.3
399	399	396	386.5	382	381	375	366	360	270	237	229.5	222	210	201.5	201.5	201.5	194	186	165	165	165	164	164	164	164	162	136	122	122	122		115.5	110
12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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AFABP; adipocyte fatty acid binding protein; atherosclerotic lesion; lesion formation inhibition; macrophage; adipocyte; atherosclerosis; serum cholesterol; therapy; human.
                                                                                                                                                                                                                                                                 Hotamisligil GS;
                  AAY90320 standard; Protein; 132 AA
                                                                              Human AFABP protein sequence.
                                                                                                                                                                                                     11-FEB-2000; 2000WO-US03560.
                                                                                                                                                                                                                         99US-0119880
                                                           (first entry)
                                                                                                                                                                                                                                            (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                 Perrella MA,
                                                                                                                                                                                                                                                                                    2000-506094/45
                                                                                                                                                                                                                                                                                     WPI; 2000-506094/
N-PSDB; AAA37717.
                                                                                                                                                             WO200047734-A1.
                                                                                                                                                                                                                         12-FEB-1999;
                                                                                                                                           Homo sapiens.
                                                          22-NOV-2000
                                                                                                                                                                                 17-AUG-2000.
                                       AAY90320;
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 Н
        AAY90320
RESULT
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Disclosure; Page 14; 43pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG66576;
                                                                                                                                                                                                                         Sequence
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AAG66576
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                                       acid binding protein) protein sequence. The invention relates to a method for inhibiting formation of an atherosclerotic lesion comprising administering to a manneal a compound that reduces expression of adipocyte fatty acid binding protein (AFABP). The method is used to inhibit formation of atherosclerotic lesions. The method is used to inhibit compounds which can be used to inhibit formation of atherosclerotic lesions inhibition of AFABP binding to an intracellular ligand in a macrophage or adipocyte, inhibition of development of an atherosclerotic legion, inhibition of a macrophage differentiating into a foam cell or inhibition of AFABP expression in a cell. AFABP activity may be inhibited to treat atherosclerosis. Inhibiting AFABP expression or activity includes the development of atherosclerosis. Inhibiting AFABP expression or activity includes the development of atherosclerotic lesions despite a high level
                                                                                                                                                                                                                                                                                                                                                       61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVM 120
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                     1 MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AFABP; adipocyte fatty acid binding protein; atherosclerotic lesion; lesion formation inhibition; macrophage; adipocyte; atherosclerosis; serum cholesterol; therapy; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reducing expression of adipocyte fatty acid binding protein through administration of a compound is used to inhibit formation of an atherosclerotic lesion -
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                                                                                                                                                                                                                                                        Length 132;
                                                                                                                                                                                                                                                                                  Indels
                                sequence represents the human AFABP (adipocyte fatty
                                                                                                                                                                                                                                                         100.0%; Score 675; DB 21;
100.0%; Pred. No. 4.2e-71;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hotamisligil GS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY90319 standard; Protein; 132 AA.
         Disclosure; Page 14; 43pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse AFABP protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-FEB-2000; 2000WO-US03560.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-NOV-2000 (first entry)
                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HARD ) HARVARD COLLEGE
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                                                                                                                                                                                                  of serum cholesterol
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acid binding protein) protein agenence. The invention relates to a method for inhibiting formation of an atherosclerotic lesion comprising administering to a mammal a compound that reduces expression of adipocyte faity acid binding protein (AFABP). The method is used to inhibit formation of atherosclerotic lesions. The method is used to identify compounds which can be used to inhibit formation of atherosclerotic lesions through inhibition of AFABP binding to an intracellular ligand in a macrophage or adipocyte, inhibition of development of an atherosclerotic legion, inhibition of a macrophage differentiating into a foam cell or inhibition of AFABP expression in a cell. AFABP activity may be inhibited to treat atherosclerosis or to treat individuals at risk of developing atherosclerosis. Inhibiting AFABP expression or activity reduces the development of atherosclerotic lesions despite a high level
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytostatin III polypeptides that modulate growth of epithelial cells, stimulate milk production in humans and cows and promote involution of breast, for research, biological, clinical and therapeutic purposes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVM 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse; cytostatin III; cytostatic; epithelial cell growth; milk production; breast involution; cardiac myocyte hypertrophy; leukaemia; MDGI; mammary-derived growth inhibitor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 625; DB 21; Length 132;
Pred. No. 2.9e-65;
5; Mismatches 6; Indels (
sequence represents the mouse AFABP (adipocyte fatty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG66576 standard; Protein; 133 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.6%;
91.7%;
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97US-0820825.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 92.6
Best Local Similarity 91.7
Matches 121; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 AA;
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The indicated peptides and the peptides represented in AAR13560 and
       Guillian-Barre syndrome
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                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                               The invention relates to an isolated Cytostatin III polypeptide Comprising a sequence selected from amino acids 1-135, 2-135, 108-135, 129-135 and 118-125, of a sequence of 135 amino acids fully defined in the specification. The polypeptide is useful for modulating growth of epithelial cells, for stimulating milk production in humans and cows, and for promoting involution of breasts. It is also useful for treating cardiac mycoyte hypertrophy and leukaemia, and is useful for research, and bological, clinical and therapeutic purposes. The present sequence is provided in the specification for comparison studies with human cytostatin III.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; myelin; P2 protein; treatment; inflammatory polyneuritis;
Guillian-Barre syndrome; vasculitis; nerve inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.0%; Score 466; DB 22; 67.9%; Pred. No. 1.1e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Mismatches
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                                      Disclosure; Fig 2; 31pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 67.9
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human myelin P2 protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Weishaupt A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | ||| ||:
|121 gsvvstrtyek ||31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 KGVTSTRVYER 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-120772/11.
N-PSDB; AAV10405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AKW40227
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61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVM 120
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                 1 MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
                                          The present sequence is the human myelin P2 protein, which can be used to treat T-cell mediated diseases of the peripheral nervous system, especially chronic-inflammatory polymeuritis, or system, especially chronic-inflammatory polymeuritis or distinct the syndrome, vasculitts and nerve inflammation in cases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammary-derived Growth Inhibitor peptide(s) - and antibodies useful in biotechnology and medicine as proliferation inhibitors e.g. of carcinoma cells
                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                  Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proliferation; inhibition; mammary-derived growth inhibitor.
                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                           67.9%; Score 458; DB 19; 1
66.9%; Pred. No. 1e-45;
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/label- active_peptide
/note- "claim 11"
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/note- "claim 10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR13559 standard; protein; 131 AA.
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Disclosure; Fig 4; 14pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 2; 6pp; German.
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                                                                                                                                                                                                                                                          Query Match 67.9°
Best Local Similarity 66.9°
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MDGI active peptides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 KGVTSTRVYE 130
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121 kgvvctriyd 130
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                                                                                                                                                                                       136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GROS/) GROSSE R.
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sequence is provided in the specification for comparison studies with \ensuremath{\mathsf{human}} cytostatin III.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG66577
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       S S X S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytostatin III polypeptides that modulate growth of epithelial cells, stimulate milk production in humans and cows and promote involution of breast, for research, biological, clinical and therapeutic purposes -
          2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVMKG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                       3 DAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTE 62
                                                                                                                                                                                                                                                                                                                                                                                                   AAR13561 are used for the production of antibodies. These are use study the mechanism of action of MDGI and related proteins and to identify new regulators active in the same way.

The peptides are synthesised by usual chemical methods and coupled to a carriter. The resulting conjugate is used to immunise animals and recovered sera tested for reactivity against antigens immobilised on nitrocellulose.
                                                                              coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        milk production; breast involution; cardiac mycyte hypertrophy; leukaemia; MDGI; mammary-derived growth inhibitor.
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0
                                                                                                                                                                                                                                                                            Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; cytostatin III; cytostatic; epithelial cell growth;
                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                    ; Score 453; DB 12;
; Pred. No. 3.7e-45;
15; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG66578 standard; Protein; 133 AA.
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                                                                                                                                                                                                                                                                         67.18;
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97US-0820825.
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                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human MDGI polypeptide
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                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 VTSTRVYER 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 avctrvyek 130
                                                                                                                                                                                                131 AA;
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                                                                                                                                                                                                                                                                       Query Match
Best Local Simi
Matches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US6232291-B1
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19-MAR-1997;
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                                                                                                                                                                                                     Sequence
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The invention relates to an isolated Cytostatin III polypeptide comprising a sequence selected from amino acids 1-135, 2-135, 108-135, 129-135 and 118-125, of a sequence of 135 amino acids fully defined in the specification. The polypeptide is useful for modulating growth of epithelial cells, for stimulating milk production in humans and cows, and for promoting involution of breasts. It is also useful for treating cardiac myocyte hypertrophy and leukaemia, and is useful for research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytostatin III polypeptides that modulate growth of epithelial cells, stimulate milk production in humans and cows and promote involution of breast, for research, biological, clinical and therapeutic purposes -
                                                                                                                                                                                    61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVM 120
                                                                                                       1 MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
                                                                                                                     Bovine; cytostatin III; cytostatic; epithelial cell growth; milk production; breast involution; cardiac myocyte hypertrophy; leukaemia; MDGI; mammary-derived growth inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and biological, clinical and therapeutic purposes. The present sequence is provided in the specification for comparison studies with human cytostatin III.
                                                                         0
                                                                           30;
                                            Score 449; DB 22;
Pred. No. 1.1e-44;
                                66.5%; Sco...
64.9%; Pred. No. 1...
16; Mismatches
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                                                                                                                                                                                                                                                                                                                                            AAG66577 standard; Protein; 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0307817.
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97US-0820825.
                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovine MDGI polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gentz R,
                                                                                                                                                                                                                                   121 KGVTSTRVYER 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-342775/36.
                                                                                                                                                                                                                                                                  121 gtavctrtyek 131
                                          Query Match
Best Local Similarity
Matches 85; Conserv
133 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US6232291-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-MAY-1999;
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 Seguence
                                                                                                                                                                                                                                                                                                                                                                           AAG66577;
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133 AA;

Sequence

61 TEISFILGOEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVM 120

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                                                                                               61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVM 120
                                                                                                          Gaps
                                                 9
                                                            The present sequence is the bovine myelin P2 protein, which can be used to treat T-cell mediated diseases of the peripheral nervous system, especially chronic-inflammatory polyneuritis, Guillian-Barre syndrome, vasculitis and nerve inflammation in cases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant myelin proteins for treating T-cell mediated disease of peripheral nervous system - by high dose antigen therapy, causing apoptosis in T cells, for treating e.g. polyneuritis or 6011lian-Barre syndrome
                                                MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN
                                                                                                                                                                                                                                                                                                                                 Bovine; myelin; P2 protein; treatment; inflammatory polyneuritis; Guillian-Barre syndrome; vasculitis; nerve inflammation;
                         ö
  Length 133;
                         31; Indels
k; Score 446; DB 22;
k; Pred. No. 2.5e-44;
15; Mismatches 31;
                                                                                                                                                                                                                                AAW40228 standard; Protein; 136 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 4; 14pp; German.
66.1%;
64.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-DE01535
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                                                                                                                                                                                                                                                                                (first entry)
                      85; Conservative
                                                                                                                                                                                                                                                                                                         Bovine myelin P2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Weishaupt A;
                                                                                                                                              121 KGVTSTRVYER 131
                                                                                                                                                              || ||:
121 gtavctrtyek 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (WEIS/) WEISHAUPT A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-120772/11.
          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GOLD R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gammopathy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUL-1996;
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                                                                                                                                                                                                                                                                                                                                                         gammopathy.
                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus.
                                                                                                                                                                                                                                                          AAW40228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
Query Match
Best Local
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The present sequence is porcine heart-fatty acid binding protein (H-FABP). The H-FABP gene can be used to localise, identify or mark porcine genes, alleles or quantitative trait loci, especially where these are associated with production traits. Alleles of the porcine H-FABP gene can be marked, allowing them to be distinguished, preferably by detection of specific restriction is tes, e.g. MSDI. HaerIII or HinfI. The H-FABP gene can also be used to localise, identify or mark genes, alleles or quantitative trait loci in samples by amplification of specific genomic fragments. By using samples large numbers of plgs can be genotyped rapidly. The methods can be used to identify differences between plg alleles associated with improvements in production traits, and in marker assisted identification/selection of pigs. The H-FABP gene can also be used to generate transgenic animals encoding desirable alleles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of H-FABP, to enhance production or physiological characteristics. Specific allelle proteins or peptides may also be produced from the agene. Such peptides, or antibodies directed against them, can be used to influence production traits in live animals or cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pig heart fatty acid-binding protein gene – used to identify polymorphisms associated with production traits, e.g. body weight,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               culture, or in diagnostic tests to select animals expressing desired forms of allelic proteins/fragments. Far reduction is desirable in pig breeding because of interest in lean meat, but previous efforts to reduce backfat deposits have also decreased
                                                                                                                                                  Porcine; pig; swine; heart-fatty acid binding protein; H-FABP; localisation; identification; marking; gene; allele; quantitative trait locus; production trait; transgenic animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INST DIERHOUDERIJ EN DIERGEZONDHEID ID-D. NOORD NEDERLANDS VARKENSSTAMBOEK BV.
                                                                                                               Porcine heart-fatty acid binding protein.
AAW31534 standard; Protein; 134 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                          96EP-0200855.
                                                                                                                                                                                                                                                                                                                                                                        97WO-NL00157
                                                                           20-APR-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   DALLAND BV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           intramuscular fat
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                                                                                                                                                                                                                 fat reduction.
                                                                                                                                                                                                                                                                                          W09735878-A2.
                                                                                                                                                                                                                                                                                                                                                                        27-MAR-1997;
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Gaps

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27; Indels

;; Score 445; DB 19; ;; Pred. No. 3.3e-44; 17; Mismatches 27;

65.9%; 66.2%;

Query Match 65.9% Best Local Similarity 66.2% Matches 86; Conservative

Length 136;

1 MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60

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                                                                                                                                                                                                                                                                    1 MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
                                                                                                                                                                                                                                                                                    Human cytostatin II DNA and protein sequence - used to modulate cellular growth and differentiation, used in the treatment of cancer
intramuscular fat (IMF), important for taste. The H-FABP gene is a muscle specific candidate for the putative gene for IMF deposition in plus gene is responsible for variation in this gene is responsible for variation in IMF % and backfat thickness, and will affect other production in traits, e.g. average daily weight gain and feed efficiency, since fat production and deposition is energy consuming, detracting energy from other purposes, e.g. analysis of body weight (BW) and IMF in relation to 3 polymorphisms in H-FABP, Mspl, HaeIII and Hiff, by Statistical Analysis System (SAS) statistics programme showed a significant difference in BW, and a distinct but not significant difference in BW, and a distinct but not
                                                                                                                                                                                                                                                                                                                                            DB 18; Length 134;
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                                                                                                                                                                                                              64.5%; Score 435.5; DB 1:
64.4%; Pred. No. 4.2e-43;
                                                                                                                                                                                                                                        15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW22408 standard; Protein; 132 AA.
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                                                                                                                                                                                                                                        85; Conservative
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N-PSDB; AAT74751.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cytostatin II
                                                                                                                                                                                                                           Similarity
                                                                                                                                                                     134 AA;
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Best Local S:
Matches 85,
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Human cytostatin II (AAW22408) is related by amino sequence homology to mammary derived growth inhibitor found in cattle and mice. Its amino acid sequence was deduced from a cDNA clone (AAT74751) obtd. from a foetal brain library. Recombinant cytostatin II can be expressed in prokaryotic or eukaryotic host cells. It can be used

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TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVM 120
                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated human fatty acid binding protein - used to develop products for treating, e.g. spina bifida, anaemia, glaucoma, seizure disorders, epilepsy and cerebrovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is the amino acid sequence of the human fatty acid binding protein (Hu-FABP) used in the method of the invention. The Hu-FABP plays a role in developmental disorders and cellular development and differentiation, including cancers. The Hu-FABP can be used for treating developmental disorders, e.g. spina bifida, hydrocephalus, and hereditary neuropathies such as Charcot-Marie-Tooth disease and neurofibromatosis. Antagonists to the Hu-FABP can be used for treating a disorder associated with cellular development and differentiation, e.g. hyperaldosteronism, and cancers including
                                                                                                                                                                                                                        1 MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
to inhibit growth and differentiation of tumour cells, or venous endothelial cells to prevent, slow or alter angiogenesis. It also inhibits mammary pothelial cell growth and modulates mammary gland differentiation and may be used to aid milk production in human mothers or to modulate breast size e.g. after parturition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; fatty acid binding protein; Hu-FABP; developmental disorder;
cancer; spina bifida; hydrocephalus; hereditary neuropathy;
Charcot-Marie-Tooth disease; neurofibromatosis; antagonist;
                                                                                                                                                                                                                                          Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of the human fatty acid binding protein
                                                                                                                                               59.1%; Score 399; DB 18;
56.8%; Pred. No. 7.6e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hyperaldosteronism; adenocarcinoma.
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                                                                                                                                                                                          Conservative
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121 gdvvavrhyeka 132
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                                                                                                                                                                      Local Similarity
nes 75; Conserv
                                                                                                       132 AA;
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                                                                                                        Sequence
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Matches
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     as
                                                                                                                                                                                             61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVM 120
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teisfqlgeefdettaddrncksvvsldgdklvhiqkwdgketnfvreikdgkmvmtltf 120
                                                                                                                   Gaps
                                                                                                                                                          1 MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
 adenocarcinoma, in particular, cancers of neurological origin such ecancers of the breast and kidney. The products can also be used for detection, diagnosis and drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated human cytostatin II - used to develop products for the treatment of e.g. cancers or viral or microbial infections or for protecting nervous system cells from toxic agents
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                                                                                         Length 132;
                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytostatin; cell growth; tumour; nervous system;
viral infection; microbial infection.
                                                                                       59.1%; Score 399; DB 19;
56.8%; Pred. No. 7.6e-39;
iive 21; Mismatches 36;
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(LONG-) LONG ISLAND JEWISH MEDICAL CENT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0041645
                                                                                                                 75; Conservative
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121 gdvvavrhyeka 132
                                                                                                                                                                                                                                              121 KGVTSTRVYERA 132
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                                                                                                                                                                                                                                                                                                                                                                                                                Human cytostatin II.
                                                                                       Query Match
Best Local Similarity
                                                  132 AA;
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haematopoiesis indicates a possible immunosuppressive activity or a lineage specific stimulation of haematopoiesis which could be used for treating conditions requiring immunosuppression. Antagonists to cytostatin II may be used in vivo to induce deficiencies or enhancement in the immune or in the haematopoietic systems. They may be used e.g. to treat cardiac myocyte hypertrophy or leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents a novel human 14-16 kDa FABP protein analogue, GEN 128B10. The gene is useful for the detection of gene expression in various tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                    61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                     1 MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
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                                                                                                                                                                                                                                  Length 132;
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                                                                                                                                                                                                                                                                               36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human 14-16 kDa FABP analogue GEN 128B10 protein.
                                                                                                                                                                                                                               59.1%; Score 399; DB 19; 56.8%; Pred. No. 7.6e-39; ive 21; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.1%; Score 399; DB 20; 56.8%; Pred. No. 7.6e-39; ive 21; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detection of its expression in tissues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97JP-0096908.
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                                                                                                                                                                                                                               Query Match 59.1
Best Local Similarity 56.8
Matches 75; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 gdvvavrhyeka 132
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Matches 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-0CT-1998.
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                                                                                                                                                                 Sequence
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AAG66580 standard; Protein; 131 AA.

AAG66580

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Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
gene therapy; chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs different from fittal human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed CDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ords in therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                      TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 13; SEQ ID 7928; 71pp + CD-ROM; English
                                                                                                                                                                                                                                                                                                            SEQ ID NO: 7928.
                                                                                                                                                                                                AAG03847 standard; Protein; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dumas Milne Edwards J, Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0122487
                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                            Human secreted protein,
                                                                      121 KGVTSTRVYERA 132
                                                                                                        121 gdvvavrhyeka 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAC03853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                            5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                 EP1033401-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-1999;
                                                                                                                                                                                                                                                                     06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-SEP-2000.
                                                                                                                                                                                                                                   AAG03847;
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                                   61
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Cytostatin III polypeptides that modulate growth of epithelial cells, stimulate milk production in humans and cows and promote involution of breast, for research, biological, clinical and therapeutic purposes -

Disclosure; Fig 2; 31pp; English.

PJ;

Dillon

Gentz R,

Yu G,

Ni J,

WPI; 2001-342775/36.

(HUMA-) HUMAN GENOME SCI INC.

96US-0013655. 97US-0820825. 99US-0307817.

10-MAY-1999; 19-MAR-1996; 19-MAR-1997;

15-MAY-2001.

Human; cytostatin III; cytostatic; epithelial cell growth; milk production; breast involution; cardiac myocyte hypertrophy; leukaemla; cytostatin II.

Homo sapiens US6232291-B1.

Human cytostatin II polypeptide.

(first entry)

22-OCT-2001

AAG66580;

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The invention relates to an isolated Cytostatin III polypeptide comprising a sequence selected from amino acids 1-135, 2-135, 108-135, 129-135 and 118-125, of a sequence of 135 amino acids fully defined in the specification. The polypeptide is useful for modulating growth of epithelial cells, for stimulating milk production in humans and cows, and for promoting involution of breasts. It is also useful for treating cardiac myocyte hypertrophy and leukaemila, and is useful for research, and blological, clinical and therapeutic purposes. The present sequence is provided in the specification for comparison studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 386.5; DB 2
; Pred. No. 2.2e-37;
20; Mismatches 36
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56.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       with human cytostatin III.
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120 gdvvavrhyeka 131
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Search completed: January 24, 2002, 09:15:21

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58.7%; Score 396; DB 21; Length 117; 69.1%; Pred. No. 1.4e-38; tve 13; Mismatches 21; Indels (

Query Match
Best Local Similarity 69.1%
Matches 76; Conservative

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1 MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60

TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTIKRKRE 110

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Job time: 428 sec

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Sequence Sequence Appli Appli Appli Appli Appli Appli Appli

Sequence 4, Sequence 11, Sequence 11, Sequence 9, Sequence 9, Sequence 8, Sequence 8, Sequence 6, Sequence 8, Sequence 3, Sequence 4,

Sequence 8, 2 Sequence 12, Sequence 12,

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1 MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
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;; Pred. No. 5.3e-49;
15; Mismatches 27; Indels
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COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,731A
FILING DATE: 24-MR-1995
CIASSIFICATION (435)
ATTORNEY/AGENT INFORMATION:
NAME: Benson, ROBERT # PF175
TELECOMMUNICATION NUMBER: PF175
TELECOMMUNICATION INFORMATION:
TELEFAX: 301-309-8504
TELEFAX: 301-309-8512
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
TWATH: 131 amino acids
                                                                                          US-08-468-709B-11
US-08-241-664B-11
US-08-470-29B-9
US-08-409-731A-9
US-08-409-731A-8
US-08-847-724-4
US-09-021-073A-8
US-09-021-073A-8
US-09-031-3
US-09-031-4
US-08-899-031-4
US-08-899-031-4
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                                                US-08-241-664B-4
PCT-US93-03936-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: NI, Jian
APPLICANT: NI, Jian
APPLICANT: Vu, Guo-Liang
APPLICANT: Reiner
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: CYTOSTATIN I
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KBY WEST AVENUE
CITY: ROCKVILLE
STRATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08409731A Patent No. 5658758
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Best Local Similarity 67.9%;
Matches 89; Conservative 11
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear;
MOLECULE TYPE: protein
US-08-409-731A-7
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237.066 Million cell updates/sec
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Sequence 11,
Sequence 7,
Sequence 11,
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Sequence 15,
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/cgn2_6/ptodata/2/laa/pcTUS_COMB.pep:*
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Compugen Ltd.
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US-08-409-731A-11
US-08-470-298B-11
US-09-0361-737-11
US-08-409-731A-10
US-08-409-731A-10
US-08-820-825-13
US-09-023-073A-10
US-09-307-817-13
US-09-307-817-12
US-08-820-825-12
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US-08-446-600A-4
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US-09-023-073A-7
US-09-307-817-11
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                 GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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1 MCDAFVGTWKLVSSENFDDY.
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Match Length DB
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                                                                                                                                                                                                                                            Title:
Perfect score:
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386.5
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Minimum DB Maximum DB

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Result 8

Searched:

Sequence:

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RESULT 3
US-08-820-825-11
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                                                    1 MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MADAFVGTWKLVDSKNFDDYMKSLGVGFATRQVASMTKPTTIIEKNGDTITIKTQSTFKN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.0%; Score 466; DB 2;
67.9%; Pred. No. 5.3e-49;
iive 15; Mismatches 27
                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: HUMAN GENOME SCIENCES, INC. STREET: 9410 KEY WEST AVENUE CITY: ROCKVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: BROOKES, ALLAN A.
REGISTRATION NUMBER: 36,373
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: CYTOSTATIN I NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                Sequence 7, Application US/08470298B Patent No. 5844081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MDGI (FIGURE 2)
                                                                                                                                                                                                                                                                                    APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: YU, GUO-LIANG
APPLICANT: ROSEN, CRAIG A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR EGG ID NO: 'SEQUENCE CHARATEON FOR EGG ID NO: 'SEQUENCE CHARATERISTICS: LENGTH: 131 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 67.9%
Matches 89; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                           | ||| ||:
121 GSVVSTRTYEK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GSVVSTRTYEK 131
                                                                                                      121 KGVTSTRVYER 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20850
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US-08-470-298B-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: MI
COUNTRY:
                                                                                                                                                                                                             US-08-470-298B-7
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61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTIIKRKREDDKLVVECVM 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 466; DB 2;
Pred. No. 5.4e-49;
                                                   APPLICANT: NI, JIAN
APPLICANT: YU, GUO-LIANG
APPLICANT: YU, GUO-LIANG
APPLICANT: DILLON, PATRICK
TITLE OF INVENTION: CYTOSTATIN III
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15; Mismatches
                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/09023073A Patent No. 5977309 GENERAL INFORMATION:
Sequence 11, Application US/08820825; Patent No. 5945309; GENERAL INFORMATION: APPLICANT: YU, JIAN APPLICANT: YU, GUO-LIANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PF2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 19-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ni, Jian
APPLICANT: Gentz, Reiner
APPLICANT: Yu, Guo-Liang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rosen, Craig
TITLE OF INVENTION: Cyto
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GSVVSTRTYEK 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 20850
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US-09-023-073A-7
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1 MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/361,737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.0%; Score 466; DB 4;
67.9%; Pred. No. 5.4e-49;
tive 15; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ni, Jian
APPLICANT: Rentz, Reiner
APPLICANT: Gentz, Reiner
APPLICANT: Tu, Guo-Liang
APPLICANT: Rosen, Craig A
TITLE OF INVENTION: Cytostatin I
CORRESPONDENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
                             US/09/307,817
                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/820,825
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/023,073
FILING DATE: 13-FEB-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                 ATONREY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF22;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/09361737 Patent No. 6287812 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 67.98
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-09-307-817-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GSVVSTRTYEK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 KGVTSTRVYER 131
                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MARYLAND: USA
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                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;; Score 466; DB 2; Length 133;
;; Pred. No. 5.4e-49;
15; Mismatches 27; Indels
                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,073A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patentin Release #1.0, Version #1.30
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: HUMAN GENOME SCIENCES, INC. 9410 KEY WEST AVENUE
                                                                                                                                                                                                                                    Sequence 11, Application US/09307817
Patent No. 6232291
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER L.
APPLICANT: DILLON, PATRICK
TITLE OF INVENTION: CYTOSTATIN III
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, 1
                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Wales, Michele M.
REGISTRATION NUMBER: P-43.975
REFERENCE/DOCKET NUMBER: PF175D:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5772
TELEFAX: 301-309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 67.9%;
Matches 89; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 133 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-09-023-073A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                         STATE: MARYLAND
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino a STRANDEDNESS:
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US-09-307-817-11
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27; Indels

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61 TEISFKLGGEFEETTADNRKTKSIVTLQRGSLNQVQRWDGKETTIKRKLVNGKWVAECKM 120
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                                                                                                                                                                      1 MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 132;
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                                                                                                      26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,298B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                             ;; Score 463; DB 1;
;; Pred. No. 1.2e-48;
17; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.6%; Score 463; DB 2;
1larity 67.2%; Pred. No. 1.2e-48;
Conservative 17; Mismatches 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 11, Application US/08470298B
; Patent No. 5844081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: YU, GUO-LIANG
APPLICANT: ROSEN, CRAIG A.
ATTILE OF INVENTION: CYTOSTATIN I
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: MYELIN P2 (FIGURE 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ALLAN A.
REGISTRATION NUMBER: 36,373
REFERENCE/CDCKET NUMBER: PF17
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 301-309-8512
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein ORIGINAL SOURCE:
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|21 KGVVCTRIYEK 131
                                                                                                                                                                                                                                                                                                                  121 KGVTSTRVYER 131
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Best Local Similarity
Matches 88; Conserva
                                                           Query Match
Best Local Similarity
Matches 88; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: NI, JI
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  US-08-409-731A-11
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US-08-470-298B-11
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
                                                                                                                                                                                                                                                                                                                                                                                                                           1 MADAFVGTWKLVDSKNFDDYMKSLGVGFATRQVASMTKPTTIIEKNGDTITIKTQSTFKN 60
                                                                                                                                                                                                                                                                                                                69.0%; Score 466; DB 4; Length 133; 67.9%; Pred. No. 5.4e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTE: Z050

COMPUTE: FLOPPY disk

COMPUTE: FLOPPY disk

COMPUTE: IBM PC compatible

OPERATIG SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/409,731A

FILING DATE: 24 MAR.1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: BENENCE/DOCKET NUMBER: 30,446

REGISTRATION NUMBER: 30,446
                                                                                                                                                                                                                                                                                                                                                          15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 9410 KEY WEST AVENUE CITY: ROCKYLLE STATE: MD
STATE: MD
STATE: MD
STATE: MD
REGISTRATION NUMBER: P-43,975
REPRENCE/OCKET NUMBER: PR175D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ni, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Yenca, Reiner
APPLICANT: Rosen, Craig A.
TILLE OF INVENTION: CYTOSTATIN I
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/08409731A Patent No. 5658758 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 301-309-8512
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                          TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 amino acids
                                                                                                                                                                                                                                                                                                                               Best Local Similarity 67.9%
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-09-361-737-7
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                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-409-731A-11
                                                                                                                                                                                                                                                                                                                Query Match
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11, Application US/09361737
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Sequence 11, Applicat Patent No. 6287812 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-361-737-11
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APPLICANT:
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                                 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVM 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,073A
FILING DATE: 13-FEB-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 68.6%; Score 463; DB 2; Best Local Similarity 67.2%; Pred. No. 1.2e-48; Matches 88; Conservative 17; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: HUMAN GENOME SCIENCES, INC. STREET: 9410 KEY WEST AVENUE CITY: ROCKVILLE STATE: MAXLAND COUNTRY: USA
                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Mi, Jian
APPLICANT: Gentz, Reiner
APPLICANT: Yu, Guo-Liang
APPLICANT: Yu, Guo-Liang
APPLICANT: Rosen, Craig A
TITLE OF INVENTION: Cytostatin I
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Wales, Michele M.
REGISTRATION NUMBER: P-43,975
REFERENCE/DOCKET NUMBER: PF175D2
TELEPHONICATION INFORMATION:
TELEPHONE: 301-610-5772
TELEPHONE: 301-610-5772
                                                                                                                                                                                                                   Sequence 11, Application US/09023073A
Patent No. 5977309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                           121 KGVVCTRIYEK 131
                                                                                      121 KGVTSTRVYER 131
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US-09-361-737-11 RESULT 10

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61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVM 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.6%; Score 463; DB 4; Length 132; 67.2%; Pred. No. 1.2e-48; Live 17; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PO-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/361,737
APPLICANT: N1, Jian
APPLICANT: Gentz, Reiner
APPLICANT: Gentz, Reiner
APPLICANT: Rosen, Craig A
TITLE OF INVENTION: Cytostatin I
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSES: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
CITY: MARYLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 09/023,073
FILING DATE: 13-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Walles, Michele M.
REGISTRATION NUMBER: 9-43,975
REFERENCE/DOCKET NUMBER: PF175D2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-409-731A-10
; Sequence 10, Application US/08409731A
; Patent No. 5658758
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                        COUNTRA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
TOWNTER: IBM PC COMPATIBLE
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Yu, Guo-Liang
Gentz, Reiner
Rosen, Craig A.
NVENTION: CYTOSTATIN I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5772
TELEFAX: 301-309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 132 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 67.24
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gentz, Re-
APPLICANT: Rosen, Cri
TITLE OF INVENTION: (
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||| ||| ||:||:
121 KGVVCTRIYEK 131
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61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TEISFKLGVEFDETTADDRKVKSIVTLDGGKLVHLQKWDGQETTLVRELIDGKLILTLTH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MYDAFLGTWKLVDSKNFDDYMKSLGVGFATRQVASMTKPTTIIEKNGDILFLKTHSTFKN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; DB 2; Length 133; 6.3e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,825 FILING DATE: 19-MAR-1997
APPLICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.5%; Score 449; 64.9%; Pred. No. 6
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Fatent No. 5945309
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: YU, GUO-LIANG
APPLICANT: DILLON, PATRICK
TITLE OF INVENTION:
UMBER OF SEQUENCES: 15
         OG-JUN-1995
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ALLAN A.
REGISTRATION NUMBER: 36,373
REPRENCE/DOCKET NUMBER: PF175
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8512
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
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US-08-470-298B-10
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                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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Best Local Similarity
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                                                                                             CLASSIFICATION:
                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20850
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US-08-820-825-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TEISFKLGVEFDETTADDRKVKSIVTLDGGKLVHLQKWDGQETTUVRELIDGKLILTLTH 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,731A FILING DATE: 24 MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.5%; Score 449; DB 1;
64.9%; Pred. No. 6.3e-47;
iive 16; Mismatches 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: HUMAN GENOME SCIENCES, INC. STREET: 9410 KEY WEST AVENUE CITY: ROCKVILLE
                                                                                                                                             COUNTR:
2IP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Ploppy disk
MED
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APPLICANT: GENTZ, REINER
APPLICANT: YU, GUO-LIANG
APPLICANT: YOSEN, CRAIG A.
TITLE OF INVENTION: CYTOSTATIN I
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/08470298B Patent No. 5844081
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RECISTRATION NUMBER: 30,446
RECISTRATION NUMBER: 30,446
REFERENCE/DOCKET UNBER: PFI
TELECOMMUNICATION:
TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 64.9%
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 301-309-8512 mot REAX: 301-309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                STREET: 9410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                  121 KGVTSTRVYER 131
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Best Local Similarity
Matches 85; Conserva
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       Best Local Similarity
Matches 85; Conserv
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 133;
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APPLICATION NUMBER: US/09/023,073A FILING DATE: 13-FEB-1998 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                          ; Score 449; DB 2;
; Pred. No. 6.3e-47;
16; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MARVITE
CONTROL
CO
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NAME: Walles, Michele M.
REGISTRATION NUMBER: P-43 975
REFERENCE/DOCKET NUMBER: PF175D2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/09023073A Patent No. 5977309 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ni, Jian
APPLICANT: Gentz, Reiner
APPLICANT: Yu, Guo-Liang
APPLICANT: Rosen, Craig A
TITLE OF INVENTION: Cytostatin I
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5772
TELEFAX: 301-309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 64.9%;
Matches 85; Conservative 16
TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS:
                                                                                                LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-820-825-13
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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Score 449;

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Query Match

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                                                                                                                                     61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVM 120
                                                                                   1 MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 133;
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Pred. No. 6.3e-47;
6: Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/307,817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 449; DB 4;
; Pred. No. 6.3e-47;
16; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER L.
APPLICANT: DILLON, PATRICK
TILLE OF INVENTION: CYTOSTATIN III
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
                      16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/09307817
Patent No. 6232291
GENERAL INFORMATION:
APPLICANT: NI, JIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/820,825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: BROOKES, ANDERS A. REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PFT
TELECOMMUNICATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INPORMATION FOR SEQ ID NO: 13 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.5%;
64.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                 NI, JIAN
YU, GUO-LIANG
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61 TEISFKLGVEFDETTADDRKVKSIVTLDGGKLVHLQKWDGQETTLVRELIDGKLILTLTH 120 g

121 KGVTSTRVYER 131 || ||: 121 GTAVCTRTYEK 131

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Search completed: January 24, 2002, 09:15:40 Job time: 382 sec

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January 24, 2002, 09:14:28; Search time 97.19 Seconds (without alignments) 377.104 Million cell updates/sec
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675
1 MCDAFVGTWKLVSSENFDDY......KLVVECVMKGVTSTRVYERA 132
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ptodata/2/paa/US092_COMB.pep:*
ptodata/2/paa/US093_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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otodata/2/paa/US085_COMB.pep:*
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/ptodata/2/paa/US088_COMB.pep:
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 1, Appli	Sequence 1, Appli	Sequence 4. Appli	Sequence 1, Appli	Sequence 913. App	Sequence 915. Ann	Sequence 917. App	Sequence 1429. An	Sequence 1432, Ap
SUMMARIES	a :	US-09-391-053-1	US-09-391-053A-1	US-09-503-596-4	US-09-905-235-1	US-09-760-469-913	US-09-760-469-915	US-09-760-469-917	US-09-760-469-1429	US-09-760-469-1432
	60	17	17	19	23	21		21		
	Length	132	132	132	132	136	136	136	136	136
& Ollery	re Match Length DB 1	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	675	675	675	675	675	675	675	675	675
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Sequence 1433, Ap	Sequence 1434, Ap									שׁ	,-		a)		_	a)						_	_	a)					35		17.	12,	37:	14769,	ø
-09-760-469-143	US-09-760-469-143	US-09-834-366-171	US-60-197-873-1716	US-09-503-59	US-09-699-146-17	US-60-212-66	US-09-216-665-1	US-08-825-78	PCT-US96-0369	US-09-023-07		US-08-470-298	US-09-734-036-1		8 US-08-470-298A-11	14 US-09-023-073-11	22 US-09-834-366-15504	24 US-60-197-873-15504	21 US-09-760-469-903	21 US-09-760-469-1419	1 PCT-US96-01640-10	1 PCT-US96-03697-13	8 US-08-470-298A-10	12 US-08-825-783-7	14 US-09-023-073-10	21 US-09-734-036-13	23 US-09-948-941-307	21 US-09-760-469-910	23 US-09-948-941-358	21 US-09-734-036-12	20 US-09-699-146-173	1 PCT-US96-03697-12	21 US-09-758-471-3729	22 US-09-834-366-14769	24 US-60-197-873-14769
136																																			
100.0	100.0	96.1	96.1	95.6	84.7	75.1	72.3	69.2	0.69	0.69	0.69	0.69	0.69	9.89	9.89	9.89	9.89	9.89	9.89	9.89	66.5	66.5	66.5	66.5	66.5	66.5	66.5	66.5	66.5	66.1	64.7	63.8	63.4	61.8	61.8
675	6/5	649	649	625	572	507	488	467	466	466	466	466	466	463	463	463	463	463	463	463	449	449	449	449	449	449	449	449	449	446	437	430.5	428	417	417
10	77	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Application US/09391053

GENERAL INFORMATION:

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APPLICANT: Biller, Scott A.
APPLICANT: Biller, Scott A.
APPLICANT: Biller, Scott A.
APPLICANT: Biller, Scott A.
APPLICANT: Jamil, Haris
APPLICANT: Jamil, Haris
APPLICANT: Jamil, Haris
APPLICANT: Jamil, Haris
APPLICANT: Man COMBINATION
TITLE OF INVENTION: AND COMBINATION
CURRENT FILING DATE: 1998-09-07
PRIOR FILING DATE: 1998-09-17
NUMBER OF EXD ID NOS: 1
SOFTWARE: PATOR OR SAPIENS
US OF THE ORDER OF THE ORDER OF THE ORDER OF THE ORGANISM: HOMO Sapiens
US OB-391-053-1

OURTY MATCH
MATCHS 132; CONSERVATIVE 0; Mismatches 0; Indels 0; Gaps 0;
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1 MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60

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Sequence 1, Application US/09905235
GENERAL INFORMATION:
APPLICANT: BRISTOL-MYERS SOUIBB COMPANY
11TLE OF INFORMION: METHOD FOR TREATING DIABETES EMPLOYING AN AP2 INHIBITOR AND CO
FILE REFERENCE: LA24a
CURRENT APPLICATION NUMBER: US/09/905,235
CURRENT FILING DAYE: 2001-07-13
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.0
SEQ ID NO 1.2
SEQ ID NO 1.2
                                      61 TEISFILGGEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRRREDDKLVVECVM 120
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GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT254
CURRENT FILING DATE: 2001-01-16
CURRENT PILING DATE: 2001-01-16
PLIOR application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1983
SOFTWARE: PAtentin Ver. 2.0
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100.0%; Pred. No. 2.1e-67;
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100.0%; Pred. No. 2.2e-67;
1ve 0; Mismatches 0;
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Best Local Similarity 100.
Matches 132; Conservative
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Best Local Similarity 100.
Matches 132; Conservative
                                                                                                                  CORGANISM: HOMO SAPIENS US-09-905-235-1
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US-09-760-469-913
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US-09-760-469-913
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LENGTH: 136
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US-09-905-235-1
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GENERAL INFORMATION:
APPLICANT: BRISTOL WIERS SQUIBE COMPANY
TITLE OF INVENTION: METHOD FOR TREATING DIABETES EMPLOYING AN AP2 INHIBITOR AND COM
FILE REFERENCE: LA24a
CURRENT APPLICATION NUMBER: US/09/391,053A
CURRENT FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 1
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TITLE OF INVENTION: Inhibiting formation of Artherosclerotic Lesions
FILE REPERENCE: 21509-042
CURRENT APPLICATION NUMBER: US/09/503,596
CURRENT FILIG DATE: 2000-02-11
PRIOR PAPLICATION NUMBER: 60/119,880
PRIOR FILING DATE: 1999-02-12
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ORGANISM: HOMO SAPIENS
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US-09-503-596-4
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Best Local Similarity
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LENGTH: 132
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US-09-503-596-4
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1432
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TITLE OF INVENTION: Nucleic Acids, Proteins, e
FILE REFERENCE: PT25A COURENT APPLICATION NUMBER: US/09/760,469
CURRENT FILING DATE: 2001-01-16
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GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REPERENCE: PT254
CURRENT APPLICATION UNDHER: US/09/760,469
CURRENT FILING DATE: 2001-01-16
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1429
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Matches 132; Conservative
                                                                    121 KGVTSTRVYERA 132
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US-09-760-469-1429
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US-09-760-469-1432
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Best Local Similarity
Matches 132; Conserv
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US-09-760-469-1429
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61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVM 120
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GRERAL INFORMATION:
APPLICAMY: Rosen et al.
ITILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PPZ54
CURRENT APPLICATION NUMBER: US/09/760,469
CURRENT FILING DATE: 2001-01-16
FILO application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1983
SOFTWARE: Patentin Ver. 2.0
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GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: Pr254
CURRENT APPLICATION NUMBER: US/09/760,469
CURRENT FILING DATE: 2001-01-16
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0; Mismatches 0;
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Matches 132; Conservative
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                                                        121 KGVTSTRVYERA 132
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US-09-760-469-915
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US-09-760-469-917
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Best Local Similarity
Matches 132; Conserv
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LENGTH: 136
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LENGTH: 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
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                                                                                                                                  Sequence 1433, Application US/09760469
GENERAL INFORMATION:
APPLICANT: ROSen et al.
TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ54
CURRENT APPLICATION NUMBER: US/09/760,469
CURRENT APPLICATION DATE: 2010-101-16
Prior application data removed - consult PALM or file wrapper: NUMBER OF SEQ ID NOS: 1983
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1433
LENGTH: 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: PTS4
CURRENT APPLICATION NUMBER: US/09/760,469
CURRENT FILLING DATE: 2001-01-16
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1983
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 134
LENGTH: 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rosen et al. IIILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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100.0%; Score 675; DB 21;
Best Local Similarity 100.0%; Pred. No. 2.2e-67;
Matches 132; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 675; DB 21;
Pred. No. 2.2e-67;
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100.0%; Pred. No. 6...
0; Mismatches
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; ORGANISM: Homo sapiens
US-09-760-469-1434
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              121 KGVTSTRVYERA 132
                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-469-1433
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61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVM 120
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                                                                                                                                                                                    APPLICANT: Tanaka, Hiroaki
APPLICANT: Tanaka, Hiroaki
APPLICANT: Tanaka, Hiroaki
APPLICANT: Danas Milne Edwards, Jean Baptiste
APPLICANT: Jobert, Severin
APPLICANT: Giordano, Jean-Yves
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: 81.US2.REG
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/197,873
PRIOR APPLICATION NUMBER: US 60/197,873
PRIOR APPLICATION NUMBER: US 60/197,873
NUMBER OF SEQ ID NOS: 52153
SOFTWARE: Patent.pm
SEQ ID NO 1169
LENGTH: 129
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APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Jobert, Severin
APPLICANT: Glordano, Jean-Yves
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: 81.051.PRO
CURRENT APPLICATION NUMBER: 05/60/197,873
CURRENT FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 52153
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96.1%; Score 649; DB 22;
98.4%; Pred. No. 1.7e-64;
tive 0; Mismatches 2;
                                                                                                                                   ; Sequence 17169, Application US/09834366; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 17169, Application US/60197873
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Xaa = Lys, Asn
US-09-834-366-17169
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125 KGVTSTRVYERA 136
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ORGANISM: Homo saplens
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Best Local Similarity
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US-60-197-873-17169
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LENGTH: 129
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TYPE: PRT
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TITLE OF INVENTION: Inhibiting formation of Artherosclerotic Lesions
FILE REFERENCE: 215.09-04.2
CURRENT APPLICATION NUMBER: US/09/503,596
CURRENT FILING DATE: 12000-02-11
PRIOR APPLICATION NUMBER: 60/119,880
PRIOR PILING DATE: 1999-02-12
NUMBER: OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                             Length 129;
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GENERAL INFORMATION:
GENERAL HOUGHATION:
APPLICANT: Glenn, Matthew
APPLICANT: Grigor, Murray R.
APPLICANT: Molenaar, Adrian J.
APPLICANT: Molenaar, Adrian J.
TITLE OF INVENTION: Compositions Isolated From Bovine
TITLE OF INVENTION: Mammary Gland and Methods For Their Use.
                                                                                                                                                                             Indels
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                                                                                                                                         Score 649; DB 24;
Pred. No. 1.7e-64;
0; Mismatches 2;
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LOCATION: 62

OTHER INFORMATION: Xaa = Asp,Glu
NAME/KEY: UNSURE
LOCATION: 82

OTHER INFORMATION: Xaa = Lys,Asn
US-60-197-873-17169
                                                                                                                                         96.18;
98.48;
                                                                                                                                                                        Matches 127; Conservative
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Best Local Similarity 91.7'
Matches 121; Conservative
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US-09-503-596-5
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                                                                                                                                      Query Match
Best Local Similarity
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US-09-503-596-5
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Gaps
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                                                                                                                                                                                                                                                        Length 132;
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                                                                                                                                                                                                                                                    84.7%; Score 572; DB 20;
83.3%; Pred. No. 8.1e-56;
1ive 8; Mismatches 14;
FILE REFERENCE: 1046U1
CURRENT APPLICATION NUMBER: U5/09/699,146
CURRENT FILING DATE: 2000-10-27
FRIOR APPLICATION NUMBER: US 60/162,701
PRIOR FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 262
SOFTWARE: FastSEQ for Windows Version 4.0
SSOTTWARE: 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: January 24, 2002, 09:17:45
Job time: 197 sec
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|121 NGVTATTVYERA 132
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Best Local Similarity
Matches 110; Conserv
                                                                                                                                                                             ORGANISM: Bovine US-09-699-146-172
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Sequence 1595, A Sequence 1595, A Sequence 1595, A Sequence 1236, Apple Sequence 1235, Apple Sequence 1234, Apple Sequence 15247, A Sequence 15245, A Sequence 11935, A Sequence 11933, A Sequen

Sequence:

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Searched:

Database

Result

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Sequence Sequence

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                        US-60-318 677-20

US-09-708 427-15957

US-09-708 427-15956

US-09-708 427-15956

US-09-708 427-15956

US-09-708 427-1236

US-09-708 427-1234

US-09-708 427-1234

US-09-708 427-1524

US-09-708 427-1524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 466; DB 5;
Pred. No. 2.6e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/901,436
FILING DATE: 10-Jul-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Wales, Michele M.
REGISTRATION NUMBER: P-43,975
REFERENCE/DOCKET NUMBER: PF175D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5772
TELEPHONE: 301-09-8439
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:

**RAPLICATION NUMBER: 09/361,737

**FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ni, Jian
Gentz, Reiner
Yu, Guo-Liang
Rosen, Craig A
TITLE OF INVENTION: CYPOStatin I
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/09901436 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 133 amino acids TYPE: amino acid
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67.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: MARYLAND
COUNTRY: USA
ZIP: 20850
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Best Local Similarity
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US-09-901-436-7
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January 24, 2002, 09:14:58; Search time 11.74 Seconds (without alignments) 390.957 Million cell updates/sec
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Sequence 20771, A
Sequence 20771, A
Sequence 20769, A
Sequence 21666, A
Sequence 21666, A
Sequence 21664, A
Sequence 21664, A
Sequence 2499, A
Sequence 35494, A
Sequence 35494, A
Sequence 579, Appli
Sequence 13599, A
Sequence 1359, Appli
Sequence 1359, Appli
Sequence 1369, A
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Sequence 2, Appli
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Sequence 21
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1 MCDAFVGTWKLVSSENFDDY......KLVVECVMKGVTSTRVYERA
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1: /cgn2_6/ptcdata/1/paa/USO6_NEW_COMB.pep:*

1: /cgn2_6/ptcdata/1/paa/USO6_NEW_COMB.pep:*

1: /cgn2_6/ptcdata/1/paa/USO8_NEW_COMB.pep:*

1: /cgn2_6/ptcdata/1/paa/USO8_NEW_COMB.pep:*

2: /cgn2_6/ptcdata/1/paa/USO9_NEW_COMB.pep:*

2: /cgn2_6/ptcdata/1/paa/USO9_NEW_COMB.pep:*

2: /cgn2_6/ptcdata/1/paa/USO9_NEW_COMB.pep:*

2: /cgn2_6/ptcdata/1/paa/USO9_NEW_COMB.pep:*
      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-708-427-21666
US-09-708-427-21665
US-09-708-427-21664
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US-09-708-427-20771
US-09-708-427-20770
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US-09-979-776-2
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US-09-971-187-2
US-09-901-436-9
US-09-901-436-8
US-10-017-754-328
US-09-901-436-2
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                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                     160442 seqs, 34771459 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                sw model
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Gapop 10.0 , Gapext 0.5
                                                             using
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Maximum DB seq length: 200000000
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Match Length

    protein search,

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Length 133;

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Sequence 10, Application US/09901436 GENERAL INFORMATION:
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                121 KGVTSTRVYER 131
                                    121 KGVVCTRIYEK 131
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20850
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                                                                                                     RESULT 3
US-09-901-436-10
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                                                                                                                   1 MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
                                                    1 MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
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67.2%; Pred. No. 5e-38;
ive 17; Mismatches 26; Indels
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
27;
                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: CYTOStatin I
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/901,436
FILING DATE: 10-011-2001
CLASSIFICATION: <UNKNOWN>
 Mismatches
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/361,737
FILING DATE: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Wales, Michele M.
REGISTRATION NUMBER: P-43,975
                                                                                                                                                                                                                                                                                          Sequence 11, Application US/09901436
GENERAL INFORMATION:
APPLICANT: Ni, Jian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
15;
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Yu, Guo-Liang
Rosen, Craig A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 67.29
Matches 88; Conservative
 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                       121 GSVVSTRTYEK 131
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US-09-901-436-11
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68;
 Matches
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61 TEISFKLGVEFDETTADDRKVKSIVTLDGGKLVHLQKWDGQETTLVRELIDGKLILITIH 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MYDAFLGTWKLYDSKNFDDYMKSLGVGFATRQVASMTKPTTIIEKNGDILTLKTHSTFKN 60
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                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.5%; Score 449; DB 5; 64.9%; Pred. No. 1.2e-36;
                                                                                                                                                                              ADDRESSEE: HUMAN GENOME SCIENCES, INC
STREET: 9410 KEY WEST AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/901,436
FILING DATE: 10-Jul-2001
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PF175D2 TELECOMMUNICATION INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 09/361,737 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Wales, Michele M. REGISTRATION NUMBER: P-43,975
                                                                    Rosen, Craig A
TITLE OF INVENTION: Cytostatin I
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
US-09-986-240-2
; Sequence 2, Application US/09986240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
APPLICANT: N1, Jian
Gentz, Reiner
Yu, Guo-Liang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 10
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                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FYPE: amino acid
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                                                                                                                                                                                                                                                           STATE: MARYLAND
                                                                                                                                                                                                                                CITY: ROCKVILLE
                                                                                                                                                                                                                                                                                     COUNTRY: USA
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67 LGQEFDEVT--ADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVMKGVT 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                            ADDRESSEE: HUMAN GENOME SCIENCES, INC. STREET: 9410 KEY WEST AVENUE
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38.6%; Pred. No. 6.3e-
tive 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/901,436
FILING DATE: 10-Jul-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Wales, Michele M.
REGISTRATION NUMBER: P-43,975
REFERENCE/DOCKET NUMBER: PF175D2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/361,737
                                                                                                                                                                                          Yu, Guo-Liang
Rosen, Craig A
TITLE OF INVENTION: CYTOSTAIN I
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-901-436-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION TELEPHONE: 301-610-5772
                                                                                                               Sequence 9, Application US/09901436 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 134 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                              Gentz, Reiner
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les 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         roPoloGY: linear
                                                                                                                                                                                                                                                                                                                                                   STATE: MARYLAND
                                                                                                                                                    APPLICANT: Ni, Jian
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121 GDVVAVRHYEKA 132
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                                                                           RESULT 6
US-09-901-436-9
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US-09-901-436-8
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 DAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.9%; Score 445; DB 5; Length 132; 65.1%; Pred. No. 2.8e-36; 1ve 16; Mismatches 29; Indels
                            APPLICANT: Wikstr"m, Mats
TITLE OF INVENTION: NEW NUCLEAR MAGNETIC RESONANCE SCREENING
TITLE OF INVENTION: METHOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.1%; Score 399; DB 5; Length 132; 56.8%; Pred. No. 8.1e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                               FILE REFERENCE: 13425-047001
CURRENT APPLICATION NUMBER: US/09/986,240
CURRENT FILING DATE: 2001-10-19
PRIOR PELING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: 60/243,626
PRIOR APPLICATION NUMBER: SE 0003811-7
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 8.16
21; Mismatches
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FILE REFERENCE: PF221D1
CURRENT APPLICATION NUMBER: US/09/971,187
CURRENT APPLICATION NUMBER: 09/043,646
PRIOR APPLICATION NUMBER: 09/043,646
PRIOR FILING DATE: 1998-09-09
PRIOR PILING DATE: 1998-09-09
PRIOR PILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
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Best Local Similarity 65.18
Matches 84; Conservative
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                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-986-240-2
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Best Local Similarity
Matches 75; Conserv
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US-09-971-187-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-971-187-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 2
                                                                                                                                                                                                                                                                  SEQ ID NO 2
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Length 134; 49; Indels

Score 225; DB 5; Pred. No. 6.3e-15;

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5 FVGTWKLVSSENFDDYMKEVGVGFATRK--VAGMAKPNMIISVNGDVITIKSESTFKNTE 62
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 138;
               : COMPOSITIONS AND METHODS FOR THE THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                 DB 6;
        FILE REFERENCE: 210121.478C18
CURRENT APPLICATION NUMBER: US/10/017,754
CURRENT FILING DATE: 2001-10-29
NUMBER OF SEQ ID NOS: 2004
SCFTWARE FEATSEQ for Windows Version 4.0
SEQ ID NO 328
LENGHH: 138
TYPEP: ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
                                                                                                                                                                                                                                                                                                                                       Pred. No. 1.3e-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 ISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDG---
                                                                                                                                                                                                                                                                                                                                                           23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/901,436
                                                                                                                                                                                                                                                                                                                 Score 201.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: PF175D2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 09/361,737
FILING DATE: CUknown>
ATTORNEY/AGENT INFORMATION
REGISTRATION NUMBER: P-43,975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09901436
GENERAL INFORMATION:
APPLICANT: N1, Jian
Gentz, Reiner
Yu, Guo-Liang
Rosen, Craig A
TITLE OF INVENTION: Cytostatin I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 10-Jul-2001 CLASSIFICATION: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 ELTNDGELILTMTADDVVCTRVYVR 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 RKREDDKLVVECVMKGVTSTRVYER 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                 29.9%;
32.4%;
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                           47; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: MARYLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-10-017-754-328
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-901-436-2
                                                                                                                                                                                                         TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 FTCYWKMLVNEWFEEYLRALDVNVALRKIANLLKPDKEIVQDGDHMIIRTLSTFRNYIMD 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 31.4%; Score 212; DB 5; Length 135; Best Local Similarity 35.7%; Pred. No. 1.2e-13; Matches 46; Conservative 34; Mismatches 47; Indels
                                                                                                                                                                                                                                               COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/901,436
FILING DATE: 10-Jul-2001
CLASSIFICATION: <Unknown>
                                                                                                                         ADDRESSEE: HUMAN GENOME SCIENCES, INC. STREET: 9410 KEY WEST AVENUE CITY: ROCKVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: PF175D2
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/361,737
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-901-436-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Wales, Michele M. REGISTRATION NUMBER: P-43,975
Gentz, Reiner
Yu, Guo-Liang
Rosen, Craig A
DF INVERTION: Cytostatin I
OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 328, Application US/10017754 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 301-610-5772
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
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Watanabe, Yoshihiro
Johnson, Jeffrey C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Henderson, Robert A.
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                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carter, Darrick
Fanger, Gary R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Retter, Marc W.
                                                                                                                                                                                     STATE: MARYLAND
                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 VVCKQVFKK 133
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APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THERREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILIG DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
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Sequence 20770, Application US/09708427

Sequence 20770, Application US/09708427

GENERAL INFORMATION:

APPLICART: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID:

TITLE OF INVENTION: THEREBY
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9
                                                                                                                                                                                                                                                                                                           211 RKEERESAADKMKFTNVYVKNLSEATTDD-ELKTTFGQYGSISSAVVMRDGDGKSRCFGF 269
                                                                                                                                                                                                                                ----ESTFKNTEISFILGQEFDEVTADDRKVKSTITLDGGV--LVHVQKWDGKS---- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 ----ESTFKNTEISFILGQEFDEVTADDRKVKSTITLDGGV--LVHVQKWDGKS---- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35;
                                                                                                                                                                                                           3 DAFVGTWKLVSSENFDDYM-KEVGVGFATRKVAGMAKPNMIISVNGDVITIKS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 DAFVGTWKLVSSENFDDYM-KEVGVGFATRKVAGMAKPNMIISVNGDVITIKS---
                                                                                                                                        Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 547;
                                                                                                                                                                           54; Indels
                                                                                                                                    11.0%; Score 74.5; DB 5; 25.0%; Pred. No. 7.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5;
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25.0%; Pred. No. 10,
19; Mismatches
                                                                                                                                                                       19; Mismatches
                                           ; LOCATION: 1..304
; OTHER INFORMATION: Ceres Seq. ID 1388881
US-09-620-394B-4280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
: LOCATION: 1..547
US-09-708-427-20771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-708-427-20771; Sequence 20771, Application US/09708427; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  270 VNFENPEDAARAVEALNGKKFDDK 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 ------TTIKRKREDDK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 VNFENPEDAARAVEALNGKKFDDK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Arabidopsis thaliana
                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 25.0°
Matches 36; Conservative
                   NAME/KEY: misc_feature
LOCATION: 1..304
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                                                                                                                                Query Match
Best Local Similarity
Matches 36; Conserva
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LENGTH: 547
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LENGTH.
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                                                                                                                                                                                                     2 SFSGKYQLQSQENFEAFMKAIGL------PEELIQKGKDIKGVSEIVQNGKHFK 49
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                                                                                                            Length 107;
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GENERAL INFORMATION:
APPLICANT: Lasek, Amy W.
APPLICANT: Lones, David A.
TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
FILE REPERENCE: PA-0038 US
CURRENT APPLICATION UMBER: US/09/981,353
CURRENT FILING DAVE: 2001-10-11
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 AFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDV-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 ITIKSESTFKNTEISFILGQEFDEVTADDRKVKSTITLDG 89
                                                                                                      Score 122; DB 5;
Pred. No. 4.7e-05;
0; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5;
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Pred. No. 0.18;
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orther InFormation: Incyte ID No: 1282225CD1
US-09-981-353-21
) MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-901-436-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1..304
OTHER INFORMATION: Xaa is any amino acid
                                                                                                    18.1%; Sco.
33.8%; Pre-
tive 20; 1
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26.0%;
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                                                                                                                                        23; Conservative
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                                                                                                                      Best Local Similarity
Matches 23; Conserv
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Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                      67 LGQEFDEV 74
                                                                                                                                                                                                                                                                                            67 VGVQKGEV 74
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LENGTH: 127
                                                                                                      Query Match
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US-09-815-242-13176
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13176, AP.

13176, AP.

INDERMATION:

CANT: Haselbeck, Robe.

CANT: 29kind, Judith W.

LICANT: 2ykind, Judith W.

LICANT: Trawick, John D.

PLICANT: Trawick, John D.

PLICANT: Trawick, John D.

PLICANT: Yamamoto, Robert T.

PRICANT: Yamamoto, Robert T.

PRICANT: Yamamoto, Robert T.

PRICANT: Yamamoto, Robert T.

PRICANT: APPLICATION NUMBER: 60/191,078

PRICA PILICATION NUMBER: 60/207,727

PRICA PILICATION NUMBER: 60/207,727

PRICA PILICATION NUMBER: 60/257,931

PRICA RPILICATION NUMBER: 60/2216

PRICA RPILICATION NUMBER: 60/227

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11.0%; Score 74.5; DE
Best Local Similarity 25.0%; Pred. No. 16;
Matches 36; Conservative 19; Mismatches
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SED ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20770
LENGTH: 559
                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature

: LOCATION: 1.:559

: OTHER INFORMATION: Ceres Seq. ID 1838597

0S-09-708-427-20770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -TTIKRKREDDK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 VNFENPEDAARAVEALNGKKFDDK 190
                                                                                                                                                                                                               TYPE: PRT ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 1..559
OTHER INFORMATION: Xaa is any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55
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Sequence 20769, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRACMENTS AND CORRESPONDING POLYPEPTID
TITLE OF INVENTION: THERENY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 20769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----ESTFKNTEISFILGQEFDEVTADDRKVKSTITLDGGV--LVHVQKWDGKS---- 102
                                                                                            21 MKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSEST----FKNTEISFILGQEFDEVTA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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  Length 610;
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                                                 Indels
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  DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 11.0%; Score 74.5; D
Best Local Similarity 25.0%; Pred. No. 20;
Matches 36; Conservative 19; Mismatches
11.0%; Score 74.5; Inarity 30.3%; Pred. No. 18; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 1..662
CTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..662
OTHER INFORMATION: Ceres Seq. ID 1838596
US-09-708-427-20769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: January 24, 2002, 09:18:03 Job time: 185 sec
                                                                                                                                                                                           77 DDRKVKSTITLDGGVLVHVQKWDGKSTTI 105
                                                                                                                                                                                                                         505 AVLKDRRDLSEDGVVLA-VATVDFKSQMI 532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
Query Match
Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                      US-09-708-427-20769
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

sw model using protein search, OM protein

January 24, 2002, 09:13:58; Search time 14.4 Seconds (without alignments) 698.267 Million cell updates/sec ou:

675 1 MCDAFVGTWKLVSSENFDDY......KLVVECVMKGVTSTRVYERA 132 US-09-905-235-1 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

Total number of hits satisfying chosen parameters:

219241 segs, 76174552 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

summaries Post-processing: Minimum Match 08 Maximum Match 100 Listing first 45

PIR_68:* 1: pir1:* 2: pir2:* 3: pir3:* pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		dР			SUMMARIES	
Result No.	Score	Query	Query Match Length	DB	QI	Description
1		100.0	132	-	FZHUF	fattv acid-binding
7	623	92.3	132	~	B25952	_
m	578	85.6	132	~	S57744	ţ.
4	486	72.0	132	Н	MPRB2	myelin P2 protein
Ŋ	477	70.7	133	~	A27452	fatty acid-binding
9	466	69.0	133	~	PC4011	
7	463	9.89	132	٦	MPHU2	
ω	450	66.7	132	~	JH0407	P2
σ	449	66.5	133	М	FZHUC	acid
10	448		131	П	MPB02	_
11	446	66.1	133	~	A34676	
12	425	63.0	131	7	S06479	
13	392	58.1	132	7	A49184	
14	390	57.8	132	7	152524	testis lipid bindi
15	382	57.0	132	~	156510	fatty acid binding
16	381	56.4	132	N	158161	lipid-binding prof
17	381	56.4	132	~	I48923	fatty acid-binding
18	378	56.0	132	N	S20297	
19	366	54.2	135	~	156326	
20	362	53.6	135	~	A47497	bindi
21	361	53.5	135	7	JC2201	fatty acid-binding
22	307.5		135	~	T15205	hypothetical prote
23	300.5	•	136	~	T15207	
24	256.5	38.0	137	~	T25123	
25	242.5		. 133	~	A48578	•
56	231.5		134	~	829600	fatty acid-binding
	229.5	34.0	133	~	A39818	14K fatty acid-bin
28	227	ω.	133	7	A44870	fatty acid-binding
29	227	33.6	134	~	S34717	retinol-binding pr

retinol-binding pr cellular retinol b	retinoic acid-bind retinoic acid-bind	retinoic acid-bind retinol-binding pr	retinol-binding pr	retinoic acid-bind retinoic acid-bind xCRABP - African c	cellular retinoic retinoic acid-bind fatty acid-binding
A29065 S45378 S43470	RJHU1 RJBOA	A35825 RJRTO RJHUO	S16355 S69360	A42495 RJHU2 I51265	153298 A61629 FZHUI
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134 134 134	137	137 135 135	135	138 138	139 95 132
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225 223 223				201.5 197.5	
30 31 32	. W. W. (35 37	8 6 6	444	4 4 4 4 4 4 5

ALIGNMENTS

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ij	9

fatty acid-binding protein, adipocyte - human

N;Alternate names: adipocyte lipid-binding protein (ALBP); fatty acid binding protein C;Species: Homo sapiens (man) C;Bate: 20-Dec-1989 #sequence_revision 03-May-1996 #text_change 22-Jun-1999

C; Accession: A33363
R; Baxa, C.A.; Sha, R.S.; Buelt, M.K.; Smith, A.J.; Matarese, V.; Chinander, L.L.; Bou Bjochemistry 28, 8683-8690, 1989
A; Title: Human adipocyte lipid-binding protein: purification of the protein and cloni A; Reference number: A33363; MUID: 90105397

A; Accession: A33363 A; Molecule type: mRNA A; Residues: 1-132 <BAX> A; Cross-references: GB:J02874; NID:g178346; PIDN:AAA51689.1; PID:g178347 A; Experimental source: subcutaneous fat

A Gene: GDB:FABP4
A; Gross-references: GDB:128030
A; Cross-references: GDB:128030
A; Map posttion: lp33-lp32
C; Superfamily: myelin P2 protein
C; Superfamily: myelin P2 protein
C; Keywords: blocked amino end; lipid binding; phosphoprotein
C; Keywords: blocked amino end; Cys) (in mature form) (probably acetylated) #st
F; 2.0/Alinding site: phosphate (Tyr) (covalent) #status predicted
F; 127, 129/Binding site: fatty acid (Arg, Tyr) #status predicted

Gaps .; 0 Ouery Match
100.0%; Score 675; DB 1; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.6e-54;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Mismatches

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1 MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN οy

QΩ

61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVM 120 ò

g

121 KGVTSTRVYERA 132 121 KGVTSTRVYERA 132 ò

RESULT B25952

myelin P2 protein homolog - mouse N;Alternate names: adipocyte lipid-binding protein; adipocyte P2 protein C;Species: Mus musculus (house mouse) C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 31-Dec-2000 C;Accession: B29552; PC1249; A24884; A05089; A30810; I49440; I49467 R;Phillips, M.; Djian, P.; Green, H.

mix of

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Gaps

Length 132;

P-2 protein

protein.

us-09-905-235-1.rpr

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A; Wolecule type: mRNA
A; Residues; 1-132 < NABA
A; Residues; 1-132 < NABA
A; Cross-references: GB:J03744; NID:g165657; PIDN:AAA31451.1; PID:g165658
A; Note: translation of initiator Met is not shown
B; Ishaque, A.; Hofmann, T.; Rhee, S.; Eylar, E.H.
J; Blod. Chen. 255, 1058-1063, 1980
A; Title: The NH-2-terminal region of the P2 protein from rabbit sciatic nerve myelin.
A; Reference number: A92266; MUID:80094496
                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: S57744
R;Specht, B.; Bartetzko, N.; Kuhl, H.; Franke, R.; Boerchers, T.; Spener, F. submitted to the EMBL Data Library, June 1995
A;Description: Mammary derived growth inhibitor - not a distinct protein but a A;Reference number: S57744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Jaccession: 42808 #sequence_revision 10-May-1996 #text_change 22-Jun-1999
C;Jaccession: A28081; A92266; A92372; A03145
R;Narayanan, V.; Barbosa, E.; Reed, R.; Tennekoon, G.
J. Biol. Chem. 263, 8332-8337, 1988
A;Title: Characterization of a cloned cDNA encoding rabbit myelln P-2 proteinty. Reference number: A28081; MUID:88228063
A;Reference number: A28081; MUID:88228063
                                                                                                                                                                                                                                                                                                                                                                          C.Species: Bos primigenius taurus (cattle)
C.Date: 19-Oct_1995 #sequence_revision 03-Nov-1995 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X89244; NID:g895753; PIDN:CAA61532.1; PID:g895754
C;Superfamily: myelln P2 protein
      TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13; Indels
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A;Residues: 56-72,'Q',74-83,'T',85-98,'N',100-132 <IS2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 578; DB 2;
Pred. No. 1.1e-45;
8; Mismatches 13;
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A; Residues: 2-56 <IS1>
R; Ishaque, A.; Hofmann, T.; Eylar, E.H.
J. Biol. Chem. 257, 592-595, 1982
A; Title: The complete amino acid sequence
A; Reference number: A92372; MUID: 82098098
A; Accession: A92372
                                                                                                                                                                                                                                                                                   RESULT 3
S57744
adipocyte-type fatty acid binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.6%;
84.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 84.1
Matches 111; Conservative
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|121 NGVTATRVYERA 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-132 <SPE>
                                                                                                                                                                     121 KGVTSTRVYERA
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A; Status: preliminary
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         61
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            ολ
                                                                                             A Accession: B25952
A Molecule type: DNA
A Molecule type: DNA
A; Molecule type: DNA
A; Cross-references: GB:M13385; NID:g198718; PIDN:AAA39417.1; PID:g387401
A; Cross-references: GB:M13385; NID:g198718; PIDN:AAA39417.1; PID:g387401
B; Cross-references: GB:M1385; NID:g198718; PIDN:AAA39417.1; PID:g387401
B; Cross-references: GB:M1385; NID:g198718; PIDN:AA3855; NID:g198718; PIDN:AB3855; NID:g19871717
A; Reference number: PC1248; MUID:g3191717
                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 25-35;37-51;59-88 <BAN>
A; Experimental source: mammary glans
R; Hunt, C.R.; Ro, J.H.S.; Dobson, D.E.; Min, H.Y.; Spiegelman, B.M.
Proc. Natl. Acad. Sci. U.S.A. 83, 3786-3790, 1986
A; Title: Adlpoyte P2 gene: Developmental expression and homology of 5'-flanking sequency A; Reference number: A24884; MUID:86233319
J. Biol. Chem. 261, 10821-10827, 1986
A;Title: The nucleotide sequence of three genes participating in the adipose differentia
A;Reference number: A92553; MUID:86278164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-39, Tr, 41-110, G', 112-132 < HUNN
A; Cross-references: GB:M13264; NID:9200183; PIDN:AAA39870.1; PID:9387504
A; Cross-references: GB:M13264; NID:9200183; PIDN:AAA39870.1; PID:9387504
A; Note: the authors translated the codon ACC for residue 40 as Ser
R; Bernlohr, D.A.; Angus, C.W.; Lane, M.D.; Bolanowski, M.A.; Kelly Jr., T.J.
A; Proc. Natl. Acad. Sci. U.S.A. 81, 5468-5472, 1984
A; Title: Expression of specific mRNAs during adipose differentiation: identification of A; Reference number: A05089; MUID:84298159
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A; Residues: 2-110,'G',112-132 <MAT>
R; Cook, K.S.; Huut, C.R.; Splegelman, B.M.
J. Cell Biol. 100, 514-520, 1985
A; Title: Developmentally regulated mRNAs in 3T3-adipocytes: Analysis of transcriptional A; Reference number: 149440; MUID:85105214
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A; Cross-references: GB: M28726; NID: 919492; PIDN: AAA37112.1; PID: 9191493
B; Crook, J.S.; Lucas, J.J.; Sibley, E.; Bolanowski, M.A.; Christy, R.J.; Kelly, T.J.; La Proc. Natl. Acad. Sci. U.S.A. 85, 2949-2953, 1988
A; Title: Expression of the differentiation-induced gene for fatty acid-binding protein A; Reference number: 149467; MUID: 88203618
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J. Biol. Chem. 263, 14544-14551, 1988
A;Title: Purification of murine adipocyte lipid-binding protein. Characterization as A;Reference number: A30810; MUID:89008309
A;Accession: A30810
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A;Residues: 1-110,'G',112-132 <BER>
A;Cross-references: GB:K02109; NID:g198716; PIDN:AAA39416.1; PID:g293695
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Pred. No. 8.6e-50;
5; Mismatches 6;
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Reywords: lipid binding; phosphoprotein
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91.7%;
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Best Local Similarity 91.7
Matches 121; Conservative
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C; Superfamily: myelin P2 prot
C; Keywords: libid binding: nP
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Gispecies: Mus musculus (house mouse)
Gispecies: Mus musculus (soffsul 14 Jul-1995 #text_change 13-Aug-1999
Gispecies: Musculus (1804511; 805278; PC1248
R.Treuner, M.; Rozak, C.A.; Gallahan, D.; Grosse, R.; Mueller, T.
Gene 147, 237-242, 1994
A;Title: Cloning and characterization of the mouse gene encoding mammary-derived grow A;Reference number: PC4011; MUID:95011621
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A; Residues: 16-22;32-45;54-59, XX', 62-63, X', 65-70;83-93;97-107;117-127 <JON>
A; Residues: 16-22;32-45;54-59, XX', 62-63, X', 65-70;83-93;97-107;117-127 <JON>
C; Superfamily: State in the state in t
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R; Bansal, M.P.; Medina, D.
Blochem. Biophys. Res. Commun. 191, 61-69, 1993
A; Title: Expression of fatty acid-binding proteins in the developing mouse mammary gl
             R;Kanda, T.; Iseki, S.; Hitomi, M.; Kimura, H.; Odani, S.; Kondo, H.; Matsubara, Y.;
Eur. J. Biochem. 185, 27-33, 1989
A;Title: Purification and characterization of a fatty-acid-binding protein from the
                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: stomach R; Jones; P.D.; Carne, A.; Bass, N.M.; Grigor, M.R. Biochem, J. 251, 919-925, 1988 Biochem, J. 251, 919-925, 1988 A; Title: Isolation and characterization of fatty acid binding proteins from mammary A; Reference number: S02471; WUID:88326235
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A; Residues: 1-133 <TRE>

A; Cross-references: GB:U02884; NID:g409956; PIDN:AAA61933.1; PID:g409957

R; Tweedie, S.; Edwards, Y.

R; Tweedie, S.; Edwards, Y.

R; Tweedie, S.; Edwards, Y.

A; Title: CDNA sequence for mouse heart fatty acid binding protein, H-FABB

A; Reference number: S04591; MUID:89296486
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A;Residues: 1-33,'G',35-98,'D',100-133 <TWE>
A;Cross-references: EMBL:X14961; NID:951266; PIDN:CAA33084.1; PID:951267
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A; Residues: 1-2,'ER',5-33,'G',35-98,'D',100-133
A; Cross-references: EMBL:X14961
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submitted to the EMBL Data Library, April 1989
A;Reference number: S05278
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A; Accession: S06478
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A; Molecule type: protein
A; Residues: 1-133 <KAN>
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 15-Dec-1988 #sequence_revision | A2818 #text_change 13-Aug-1999
C;Accession: A28458; A27452; A2838; A39551; A28197; S06478; S02471
R;Heuckeroth, R.O.; Birkenmeier, E.H.; Levin, M.S.; Gordon, J.I.
A; Biol. Chem. 252, 9709-9717, 1987
A;Title: Analysis of the tissue-specific expression, developmental regulation, and linka
A;Reference number: A28458; MUID:87250640
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A)Experimental source: heart
A)Sacchetthin, J.C.; Sald, B.; Schulz, H.; Gordon, J.I.
J. Biol. Chem. 261, 8218-823, 1986
A)Title: Rat heart fatty acid-binding protein is highly homologous to the murine adipocy
A)Reference number: A23838; MUID:86250713
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K; Kimura, H.; Odani, S.; Nishi, S.; Sato, H.; Arakawa, M.; Ono, T.
J. Biol. Chem. 266, 5963-5972, 1991
A; Title: Primary structure and cellular distribution of two fatty acid-binding proteins
A; Reference number: A39551; MUID:91170283
C;Comment: P2 protein and myelin basic protein together constitute a major fraction of C;Superfamily: myelin P2 protein C;Keywords: acetylated amino end; myelin; phosphoprotein C;Keywords: acetylated amino end (Ser) (in mature form) #status experimental F;2/Nodified site: phosphate (Tyr) (covalent) #status predicted F;118-125/Disulfide bonds: #status predicted
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A; Residues: 10-69, 'Q', 71-121, 'D', 123-133 <KIM>
A; Experimental source: kidney
R; Gibson, B.W.; Yu, Z.; Aberth, W.; Burlingame, A.L.; Bass, N.M.
J. Biol. Chem. 263, 4182-4185, 1988
A; Title: Revision of the blocked N terminus of rat heart fatty acid-binding protein by A; Reference number: A28197; MUID:88153733
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A)Experimental source: cardiac
R)Claffey, K.P.; Herrera, V.L.; Brecher, P.; Ruiz-Opazo, N.
Biochemistry 26, 7900-7904, 1987
A)Title: Cloning and tissue distribution of rat heart fatty acid binding A;Reference number: A27452; MUID:88107756
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Residues: 'TEKN',5-50,'YG',53-64,'N',65-70,'D',72-133 <SAC>
Experimental source: heart
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; Pred. No. 2.5e-37;
15; Mismatches 23;
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71.0%;
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Best Local Similarity 71.0%
Matches 93; Conservative
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A; Molecule type: protein
A; Residues: 2-10;46-53 <GIB>
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A; Residues: 1-133 <HEU>
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A; Molecule type: DNA
A; Readdues: 1-132 <NBS-
A; Readdues: 1-132 <NBS-
A; Cross-references: GB:S39508; NID:g232319; PIDN:AAB19249.1; PID:g232320
C; Comment: This basic protein is found in peripheral and central nervous system myeli
C; Genetics: 25/1; 82/3; 116/3
C; Superfamily: myelin P2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fatty acid-binding protein, cardiac and skeletal muscle - human N;Alternate names: fatty acid-binding protein 3 (FABP3)
C;Specias: Homo saplans (man)
C;Date: 30-Jun-1991 #sequence_revision 03-May-1996 #text_change 16-Jul-1999
C;Accession: S15432; JH0199; S00603; I54275; A27248
R;Peeters, R.A.; Veerkamp, J.H.; van Kessel, A.G.; Kanda, T.; Ono, T.
Biochem. J. 276, 203-207, 1991
A;Title: Cloning of the CDNA encoding human skeletal-muscle fatty-acid-binding protein A;Reference number: S15432; MUID:91248148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Accession: S15432
A.Molecule type: mRNA; protein
A.Rolecule type: mRNA; protein
A.Rolecule type: mRNA; protein
A.Stoss-references: EMBL:X56549; NID:931292; PIDN:CAA39889.1; PID:931293
A.Experimental source: heart muscle; skeletal muscle
R.Boerchers, T.; Hojrup, P.; Nielsen, S.U.; Roepstorff, P.; Spener, F.; Knudsen, J.
Mol. Cell. Biochem. 98, 127-133, 1390
A.Title: Revision of the amino acid sequence of human heart fatty acid-binding protein
A.Reference number: JH0199; MUID:91094793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        myelin P2 protein - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: JH0407
R;Narayanan, V.; Kaestner, K.H.; Tennekoon, G.I.
J. Neurochem. 57, 75-80, 1991
A;Title: Structure of the mouse myelin P2 protein gene.
A;Reference number: JH0407; MUID:91268811
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A;Residues: 2-129,'Q',131-133 <BOE>
*R:Offner, G.D.; Brecher, P.; Sawlivich, W.B.; Costello, C.E.; Troxler, R.F.
Blochem. J. 252, 191-198, 1988
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                                                                                               61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVM 120
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         1 MSNKFLGTWKLVSSENFDDYMKALGVGLATRKLGNLAKPTVIISKKGDIITIRTESTFKN 60
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$; Pred. No. 4.7e-34;
18; Mismatches 28,
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Best Local Similarity
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A; Reference number: PC1248; MUID:93191717
A; Accession: PC1248
A; Mocession: PC1248
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A; Mocession: PC1248
A; Mocession: PC1248
A; Residues: 23-108, 'R', 110-119 < CANA
A; Residues: 23-108, 'R', 110-119 < CANA
A; Residues: 23-108, 'R', 110-119 < CANA
A; Residues: 24-108, 'R', 110-119 < CANA
C; Residues: 24-108, 'R', 110-119 < CANA
C; Residues: 110-108, 'R', 110-119 < CANA
C; Residues: 110-
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A; Title: Isolation and sequence determination of cDNA encoding P2 protein of human perip. A; Reference number: JT0977; MUID:92068191
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A;Cross-references: EMBL:X62167; NID:g35185; PIDN:CAA44096.1; PID:g35186
A;Argerianental source: fetal spinal cord peripheral myelin
A;Argeriantal source: translate the codon for residue 1
B;Suzuki, M.; Kitamura, K.; Sakamoto, Y.; Uyemura, K.
J. Neurochem. 39, 1759-1762, 1982
A;Title: The complete amino acid sequence of human P2 protein.
A;Reference number: A03143; MUID:83058785
A;Molecule type: protein
A;Residues: 2-98,'N',100-110,'D',112-132 <SUZ>
C;Comment: P2 protein and myelin basic protein together constitute a major fraction of genetics:
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A.Map postition: 8q21.3-8q22.1
C.Superfamily: myelin P2 protein
C.Superfamily: myelin P2 protein
F:2-132/Product: myelin P2 protein #status experimental <MAT>
F:2.Modified site: acetylated amino end (Ser) (in mature form) #status experimental
F:20/Rinding site: phosphate (Tyr) (covalent) #status predicted
F:118-125/Disulfiide bonds: #status experimental
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C;Species: Homo sapiens (man)
C;Date: 05-Apr-1983 #sequence_revision 27-Jan-1995 #text_change 08-Dec-2000
C;Accession: JT0977; A03143; S24224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVM 120
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Best Local Similarity 67.2%; Pred. No. 3.1e-35;
Matches 88; Conservative 17; Mismatches 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 69.0%; Score 466; DB 2; Best Local Similarity 67.9%; Pred. No. 1.7e-35; Matches 89; Conservative 15; Mismatches 27
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A; Residues: 1-132 <HAY>
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A; Accession: JT0977

A; Gene: GDB: PMP2

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Adderence number: Manmary-derived growth inhibitor

C. Species: Bos prinagenlus taurus (catte)

A. Tetle: Developmental regulation of mammary-derived growth inhibitor expression in k

A. Reference number: Ad4676; MUID: 90243786

A. Residues: 1-133 <-KURA

A. Residues: 1-133 <-KURA

A. Residues: 1-133 <-KURA

A. Residues: T. Kratzin, H.; Hahn, U.; Hagenhoff, B.; Lezius, A.G.; Spener

Bur. J. Biochem. 175, 549-556, 1988

A. Reference number: Soll13; MUID: 88312634

A. Accession: Soll33

A. Accession: Soll33

A. Accession: Soll33

A. Molecule type: mRNA

A. Residues: 1-133 <-Bull:
A. Accession: Soll33

A. Molecule type: mRNA

A. Residues: 1-133 <-Bull:
A. Cross references: EMBL: X12710; NID: 9338; PIDN: CAA31212.1; PID: 9339

A. Experimental source: heart

A. Cross references: EMBL: X12710; NID: 9338; PIDN: CAA31212.1; PID: 9339

A. Experimental source: heart

A. Cross references: EMBL: X12710; NID: 9338; PIDN: CAA31212.1; PID: 9339

A. Experimental source: heart

A. Reference number: A1883; MUID: 90375486

A. Reference number: A37883; MUID: 90375486

A. Reference number: A37883; MUID: 90375486

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A;Note: 99-Asp was also found
B;Sobelmer, F.D.; Kraft, R; Otto, A.; Wernstedt, C.; Hellman, U.; Kurtz, A.; Mueller, J. Biol. Chem. 262, 15137-15143, 1987
A;Title: Identification of a polypeptide growth inhibitor from bovine mammary gland. A;Reference number: A29466; MUID:88033096
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                                                                                                                                                                                                 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVM 120
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                                    FILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVMKGVT
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nes 85; Conservative
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                                                                                                                   A; Molecule type: protein
A; Molecule type: protein
A; Residues: 2-104, "K', 106-124, S', 126-133 < OFF>
A; Residues: 2-104, "K', 106-124, S', 126-133 < OFF>
A; Residues: 2-104, "K', 106-124, S', 126-133 < OFF>
A; Residues: 2-104, "K', 106-124, S', 126-133 < OFF>
A; Sabotti, G.; Scapin, G.; Spadon, P.; Veerkamp, J.H.; Sacchettini, J.C.
A; Biol. Chem. 267, 18541-18550, 1992
A; Title: Three-dimensional structure of recombinant human muscle fatty acid-binding prot A; Reference number: A49251; MUD:92406763
A; Contents: annotation; X-ray crystallography, 2.1 angstroms
A; Note: recombinant protein expressed in Escherichia coli
B; TroxLer, R.F.; Offer, G.D.; Jiang, J.W.; Wu, B.L.; Skare, J.C.; Milunsky, A.; Wyandt, A; Title: Localization of the gene for human heart fatty acid binding protein to chromose
A; Reference number: 154275
A; MUD:94085953
A; Ascession: 154275
A; MUD:94085953
A; Mestduest if-ins RRAS
A; Residuest type: mRNA
A; Residuest if-ins RRAS
A; Residuest if-ins RRAS
A;Title: Characterization and amino acid sequence of a fatty acid-binding protein from A;Reference number: S00603; MUID:88339792
A;Accession: S00603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 1p33-1p32
C;Superfamily: myelin P2 protein
C;Superfamily: myelin P2 protein
C;Keywords: acetylated amino end; cardiac muscle; heart; lipid binding; phosphoprotein
F;2/Modified site: acetylated amino end (val) (in mature form) *status experimental
F;20/Binding site: phosphate (Tyr) (covalent) *status predicted
F;127,129/Binding site: fatty acid (Arg, Tyr) *status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein in bovine peripheral nerve
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Date: 31-Aug-1980 #sequence_revision 31-Aug-1980 #text_change 05-Aug-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVM 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.5%; Score 449; DB 1; Length 133; 64.9%; Pred. No. 5.9e-34; Live 16; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 67.7%; Pred. No. 7.1e-34; Similarity 67.7%; Pred. No. 7.1e-34; Sonservative 16; Mismatches 25; Indels
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R; Kitamura, K.; Suzuki, M.; Suzuki, A.; Uyemura, K.
FEBS Lett. 115, 27-30, 1980
A; Title: The complete amino acid sequence of the P2
A; Reference number: A03144; MUID:80225120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GDB:128008; OMIM:134651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 KGVTSTRVYER 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 85; Conserv
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Best Local Simi
Matches 86;
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Matches
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5 FVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVIJIKSESTFKNTEIS 64

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C:Species: Rattus norvegicus (Norway rat)
R:Schmitt, M.C.; Jamison, R.S.; Orgebin-Crist, M.C.; Ong, D.E.
R:Schmitt, M.C.; Jamison, R.S.; Orgebin-Crist, M.C.; Ong, R.; Morales, C.R.
R:Schwitte: Rattus Rattular protein, With sequence similarities to a family of lipid A; Title: A novel testicular protein, with sequence similarities to a family of lipid A; Reference number: 153089; MUD:95046905
A; Residuar preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: MRNA
A; Molecul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fatty acid binding protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 13-Aug-1999
C;Accession: 156510
R;Bennett, E.; Stenvers, K.L.; Lund, P.K.; Popko, B.
J. Neurochem. 63, 1616-1624, 1994
A;Title: Cloning and characterization of a cDNA encoding a novel fatty acid binding p
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                                       1 MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN
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A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA
A;Residues: 1-132 <RES>
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121 GDVVAVRHYEKA 132
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121 NNVVSTRTYER 131
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A; Residues: 1-131 <SCH>
A; Residues: 1-131 <SCH>
A; Experimental Source: brain
A; Note: 11-Val, 12-Asp, 14-Lys, 18-Asp, 33-Ala, 34-Ser, 40-Thr, 43-Glu, 44-Lys, 49-Val,
R; Schoentgen, F.; Bonanno, L.M.; Pignede, G.; Jolles, P.
Mol. Cell. Biochem, 98, 35-39, 1990
A; Title: Amino acid sequence and some ligand binding properties of fatty acid-binding px
A; Reference number: JH0198; WUID: 91094811
A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Exp. Eye Res. 56, 95-106, 1993
A;Title: Identification and characterization of transcripts present at elevated levels
A;Reference number: A49184; MUID:93162137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Comment: Synaptosomal Na+-dependent amino acid transport is stimulated by the fatty C;Superfamily: myelin P2 protein C;Keywords: blocked amino end (Val) (probably acetylated) #status experimental F:1/Modified site: blocked amino end (Val) (probably acetylated) #status experimental
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                                                                                                                                                                                                                                fatty acid-binding protein, brain - bovine
C;Species: Bos primiqenius taurus (cattle)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 24-Nov-1999
C;Accession: S06479; JH0198
R;Schoentgen, F.; Pignede, G.; Bonanno, L.M.; Jolles, P.
Eur. J. Biochem. 185, 35-40, 1989
A;Title: Fatty-acid-binding protein from bovine brain. Amino acid sequence and A;Reference number: S06479; MUID:90032683
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N;Alternate names: lipid-binding protein
C;Species: Gallus gallus (chicken)
C;Date: 19-Dec.1993 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C;Accession: A49184; S26599
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A;Experimental Source: retina
A;Note: sequence extracted from NCBI backbone (NCBIP:124757)
C;Superfamily: myelin P2 protein
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; Pred. No. 8.9e-29;
19; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 131;
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Pred. No. 8.8e-32;
0; Mismatches 29; Indels
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62.0%; Pre
tive 20;
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56:1%;
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Best Local Similarity 56:19
Matches 74; Conservative
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Best Local Similarity 62.03
Matches 80; Conservative
                                       || ||:
| 121 GTAVCTRTYEK 131
121 KGVTSTRVYER 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 VVAVRHYEK 130
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A; Status: preliminary
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A;Cross-references: EMBL:U02096; NID:g476081; PIDN:AAA60455.1; PID:g476082 C;Superfamily: myelin P2 protein

Query Match 57.0%; Score 385; DB 2; Length 132; Best Local Similarity 55.3%; Pred. No. 3.9e-28; Matches 73; Conservative 19; Mismatches 40; Indels

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121 KGVTSTRVYERA 132

| : | ||:| 121 GDVVAVRCYEKA 132 δy

Search completed: January 24, 2002, 09:16:01 Job time: 123 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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 protein search, using sw model OM protein January 24, 2002, 09:15:23; Search time 11.7 Seconds (without alignments) 413.654 Million cell updates/sec Run on:

US-09-905-235-1 Perfect score:

675 1 MCDAFVGTWKLVSSENFDDY......KLVVECVMKGVTSTRVYERA 132 Sednence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	P15090 homo sapien	m snm	sns	P70623 rattus norv		oryc		P11404 mus musculu	homod	_	P24526 mus musculu	homo	_	002772 sus scrofa	Q09139 bos taurus	O13008 oncorhynchu	O15540 homo sapien				P55051 rattus norv	P80049 ginglymosto		P55052 bos taurus	Q01469 homo sapien	Q05816 mus musculu	P55053 rattus norv	P82188 lampetra ja	echinococ	_		schist	P41496 schistocerc
		ID	FABA_HUMAN	FABA_MOUSE	FABA_PIG	FABA_RAT	FABA_BOVIN	MYP2_RABIT	FABH_RAT	FABH_MOUSE	MYP2_HUMAN	MYP2_BOVIN	MYP2_MOUSE	FABH_HUMAN	FABH_BOVIN	FABH_PIG	FABB_BOVIN	FABH_ONCMY	FABB_HUMAN	TLBP_RAT	FABB_CHICK	TLBP_MOUSE	FABB_RAT	FABL_GINCI	FABB_MOUSE	FABE_BOVIN	FABE_HUMAN	FABE_MOUSE	FABE_RAT	FABL_LAMJA	FABP_ECHGR	FABP_LEPDS	FABP_BLOTA	FABP_SCHMA	FABM_SCHGR
	i	e ;	H	-	Н	Н	7	-	7	٦	٦	1	-	-	П	П	1	Н		-	-			7	Η.	٦.	٦.	7	7		ч	Н	-	-	П
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æ	Ouery	Match	99.3	91.9		o,	4	H	6.69	0.69	68.0	66.4	ė	٠. د	65.5	65.5	63.0	62.8	58.5	57.8	57.5	57.2	56.4	26.0	55.9	φ.	54.2	(1)	η,	æ	40.1	7	35.3	34.0	33.6
	Č	score	670	620	608	209	573	482	472	466	459	448	446	445	442	442	425	424	395	390	388	386	381	378	377	367	366	362	361	326	270.5	250	238	229.5	227
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Gaps

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Query Match 99.3%; Score 670; DB 1; Length 131; Best Local Similarity 100.0%; Pred. No. 2.5e-53; Matches 131; Conservative 0; Mismatches 0; Indels

	P06768 rattus norv P50121 sus scrofa P29762 homo sanian				
RET2_MOUSE RET2_HUMAN	RET2_RAT RET2_PIG RET3_HUMAN	FABM_LOCMI RET3_BOVIN	RET1_RAT RET3_FUGRU	RET1_HUMAN RET1_MOUSE	RET4_MOUSE
33 1	133 133 136 136	33 1 36 1	36 1	34 1 34 1	37 1
	33.0 32.0 1				
227	223 223 222	221	218	212	206.5
4.00	36 38	39	42	44	45

ALIGNMENTS

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                                                01-APR-1990 (Rel. 14, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
FATTY ACID-BINDING PROTEIN, ADIPOCYTE (AFABP) (ADIPOCYTE LIPID-BINDING
PROTEIN) (ALBP) (A-FABP).
                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
PHOSPHORYLATION (BY TYR-KINASES)
(BY SIMILARITY).
81C241B63DD98235 CRC64;
                           131 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIMTS; PR00061; lipocalin; 1.
PRIMTS; PR00178; FATTYACIDBP.
PROSITE; PS00214; FABP; 1.
ITANSPORT; Lipid-binding; Phosphorylation.
MOD_RES 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000463; Fatty_acid_BP.
InterPro; IPR000566; Lipocln_cytFABP.
                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14588 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; J02874; AAA51689.1; -.
                          STANDARD;
                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A33363; A33363.
HSSP; P04117; 1ALB.
MIM; 600434; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 AA;
                                                                                                                                                                NCBI_TaxID=9606;
                       FABA_HUMAN P15090;
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RESULT 1
FABA_HUMAN
                                                                                                                FABP4.
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us-09-905-235-1.rsp

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TURN
01-NOV-1986 (Rel. 03, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
EATT ACID-BINDING PROTEIN, ADIPOCYTE (AFABP) (ADIPOCYTE LIPID-BINDING PROTEIN) (ALBP) (P2 ADIPOCYTE PROTEIN) (MYELIN P2 PROTEIN HOMOLOG)
(373-L1 LIPID BINDING PROTEIN) (422 PROTEIN) (P15).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-84298159; PubMed-6206497;
Bernlohr D.A., Angus C.W., Lane M.D., Bolanowski M.A., Kelly T.J. Jr.,
"Expression of specific mRNAs during adipose differentiation:
identification of an mRNA encoding a homologue of myelin P2
protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-88203618; PUDMed-2452440;
COOK J.S., Lucas J.J., Sibley E., Bolanowski M.A., Christy R.J.,
Kelly T.J. Jr., Lane M.D.;
Expression of the differentiation-induced gene for fatty acid-binding
profesh is activated by glucocorticoid and cAMP.";
Proc. Natl. Acad. Sci. U.S.A. 85:2949-2953(1988).
                                                                                                     61 EISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVWK 120
                                                                              62 EISFILGOEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVMK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phillips M., Dian P., Green H., "The nucleotide sequence of three genes participating in the adipose differentiation of 373 cells."; J. Biol. Chem. 261:10827-10827(1986).
                1 CDAFVGTWKLVSSENFDDTWKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBL_raxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-85105214; PubMed-3968175; Cook K.S., Hunt C.R., Splegelman B.M.; bevelopmentally regulated mRNAs in 3T3-adipocytes: analysis of transcriptional control."; J. Cell Biol. 100:514-520(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-8623319; PubMed-3520554; Min H.Y., Spiegelman B.M.; Hunt C.R., Ro J.H.-S., Dobson D.E., Min H.Y., Spiegelman B.M.; Adipocyte P2 gene: developmental expression and homology of 5'-flanking sequences among fat cell-specific genes."; Proc. Natl. Acad. Sci. U.S.A. 83:3786-3790(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matarese V., Bernlohr D.A.; "Purification of murine adipocyte lipid-binding protein. Characterization as a fatty acid- and retinoic acid-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 81:5468-5472(1984).
                                                                                                                                                                                                                                                                                                                           131 AA
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                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-86278164; Pubmed-3015943;
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                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                   122 GVTSTRVYERA 132
                                                                                                                                                                                              [2]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                      FABA_MOUSE
P04117;
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                                                                                                                                                                                                                                                                                                 FABA_MOUSE
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                                                                                                                                                                                                                                                                                                                           MEDLINE-93216758; PubMed-8463311;
Xu Z., Bernlohr D.A., Banaszak L.J.;
"The adipocyte lipid-binding protein at 1.6-A resolution. Crystal structures of the apoprotein and with bound saturated and unsaturated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).

BEDLINE-22207973: PubMed-1554730;

Xu Z., Bernlohr D.A., Banascak L.J.;

"Crystal structure of recombinant murine adipocyte lipid-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION (BY TYR-KINASES)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBSELLUTAR LOCATION: CYTOPLASMIC (POTENTIAL)
-1- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF TRANSPORTERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY).
N -> T (IN REF.
G -> V (IN REF.
                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:88038; AP2.
InterPro; IPR000463; Fatty_acid_BP.
InterPro; IPR000566; Lipocln_cytFABP.
Pfan; PP00061; lipocalin; 1.
PRINTS; PR00178; FATTYACIDBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, NOZICH, ARA39870.1;

EMBL, MI3264, ARA39870.1;

EMBL, MI3262, ARA39870.1;

EMBL, MI3263, ARA39870.1;

EMBL, MI3363, ARA39870.1;

EMBL, MI3365, ARA39870.1;

EMBL, MI3365, ARA37188.1;

EMBL, M2884, AA3884.

PIR, A24884, A24884.

PIR, A30810;

PIR, A30810;

PIR, 330810;

PIR, 330810;

PIR, 330810;

PIR, 330810;

PIR, 1112;

PIR, 30-APR-94.

PIR, 1112;

PIR, 1112;

PIR, 1114;

PIR, 1115;

PIR, 1116;

                                                                                                                                                                                                         Biochemistry 31:3484-3492(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; K02109; AAA39416.1; -.
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PDB; 1A18; 01-JUL-98,
PDB; 1A2D; 01-JUL-98
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110
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STRAND
HELIX
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STRAND
TURN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
FATTY ACID-BINDING PROTEIN, ADIPOCYTE (AFABP) (ADIPOCYTE LIPID-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 EISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVMK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 CDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prinsen C., Veerkamp J.H.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
PHOSPHORYLATION (BY TYR-KINASES)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN FATTY ACID AND RETINGIC ACID.
-1- SUBCELLUIAR LOCATION: CYTOPLASMIC (POTENTIAL).
-1- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 608; DB 1; Length Lo. Pred. No. 8.4e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           656CB0CA08CD4AB2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0178; FATTACIDBE.
PROSITE; PS00214; FABP; 1.
Transport; Lipid-binding; Phosphorylation...
INIT MET 0 0 PR SIMILARITY
MOD_RES 19 19 PHOSPHORYLATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 608;
                                                                                                                                                                                                                                                                                                                 InterPro; IPR000463; Fatty_acid_BP.
InterPro; IPR000566; Lipocin_cytFABP
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Matches 116; Conservative
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P70623;
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20-AUG-2001 (Rel. 40, Last annotation update)
FATTY ACID-BINDING PROTEIN, ADIPOCYTE (AFABP) (ADIPOCYTE LIPID-BINDING PROTEIN) (ALBP) (A-FABP) (A-FAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Armstrong M.K., Bernlohr D.A., Storch J., Clarke S.D.;
"The purification and characterization of a fatty acid binding protein specific to pig (Sus domesticus) adipose tissue.";
Biochem. J. 267:373-378(1990).
-i- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG CHAIN FATTY ACID AND RETINOIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVMK 121
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STRAIN-DUROC; TISSUE-Liver;
MEDLINE-99099248; Pubmed-9880671;
Gerbens F., Jansen A., van Erp A.J.M., Harders F., Meuwissen T.H.E.,
Rettenberger G.F.W., Veerkamp J.H., te Pas M.F.W.;
"The adipocyte fatty acid-binding protein locus: characterization and association with intramuscular fat content in pigs.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNT 61
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Sus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 620; DB 1; Length 131; Pred. No. 7.2e-49;
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-1- TISSUE SPECIFICITY: ADIPOSE TISSUE.
-1- PTM: THE N-TERMINUS IS BLOCKED.
-1- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Indels
                                                                                                                                                                                                                                                                                                                                                               MW; ED57D4E2774B8E32 CRC64;
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
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20-AUG-2001 (Rel. 40, Last sequ
20-AUG-2001 (Rel. 40, Last and
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91.6%;
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Best Local Simi
Matches 120;
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097788;
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Transport; L
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P02691;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
FATTY ACID-BINDING PROTEIN, ADIPOCYTE (AFABP) (ADIPOCYTE LIPID-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Mammary gland;
MEDLINE-9635529; PubMed-8702709;
Specht B., Bartetzko N., Hohoff C., Kuhl H., Franke R.,
Boerchers T., Spener F.;
Mammary derived growth inhibitor is not a distinct protein but a mix of heart-type and adipocyte-type.fatty acid-binding protein.";
J. Blol. Chem. 271:19943-19949(1996).
I- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG CHAIN FATTY ACID AND RETINDIS (BY SIMILARITY).
I- SUBCELLUTAR LOCATION: CYTODLASMIC (POTENTIAL).
I- SUBCELLUTAR BELONGS TO THE FABP/P2/CRBPF/CRABP FAMILY OF
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                    1 CDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNLIISVEGDLVVIRSESTFKNT 60
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                   ö
                                                                                  BY SIMILARITY.
PHOSPHORYLATION (BY TYR-KINASES)
                                                                                                                                                           Score 607; DB 1; Length 131;
                                                                                                                                                                                7; Indels
                                                                                                           (BY SIMILARITY).
5228DOAC14FFD23B CRC64;
                                                                                                                                                                     Pred. No. 1e-47;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        131 AA
                       InterPro; IPR000566; Lipocln_cytFABP.
Prim; PF00061; Ilpocalin; 1.
PRIMES: PR00178; FATTACIDBP.
PROSITE; PS00214; FABP; 1.
Transport; Lipid-binding; Phosphorylation.
INIT MET 0 0 BY SIMILARITY
MOD_RES 19 19 PHOSPHORYLATI
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InterPro; IPR000566; Lipocln_cytFABP.
Pfam; PF00061; lipocalin; 1.
HSSP; P04117; 1ALB.
InterPro; IPR000463; Fatty_acid_BP.
InterPro; IPR000566; Lipocin_cytFABP.
                                                                                                                      131 AA; 14577 MW;
                                                                                                                                                       Query Match 89.9%;
Best Local Similarity 88.5%;
Matches 116; Conservative 6
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                                                                                                                                                                                                                                                                                                                  taurus (Bovine).
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P48035;
                                                                                                                      SEQUENCE
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FABA_BOVIN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way monoified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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-i- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVMK 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
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                                                                                                                     (BY TYR-KINASES)
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                                                                                                                                                                                                                                                                   84.9%; Score 573; DB 1; Length 131;
84.0%; Pred. No. 1.1e-44;
ive 8; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Narayanan V., Barbosa E., Reed R., Tennekoon G., "Characterization of a cloned cDNA encoding rabbit myelin
                                                                                                                                              (BY SIMILARITY).
A7D81B036C972D68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
02-JUG-2001 (Rel. 40, Last annotation update)
MYELIN P2 PROTEIN.
                                                                                      BY SIMILARITY.
PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 AA
PRINTS; PR00178; FATTXACIDBP.
PROSITE; PS00214; FABP; 1.
Transport; Lipid-binding; Phosphorylation.
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Biol. Chem. 255:1058-1063(1980)
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MEDLINE-80094496; PubMed-7356651;
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                                                                                                                                                                             131 AA; 14547 MW;
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|121 GVTATRVYERA 131
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us-09-905-235-1.rsp

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PRELIMINARY SEQUENCE
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MEDLINE=87250640; PubMed=3036869;
MEDLINE=87250640; Dubmed=3036869;
Heuckeroth R.O., Birkenmeier E.H., Levin M.S., Gordon J.I.;
"Analysis of the tissue-specific expression, developmental regulation, and linkage relationships of a rodent gene encoding heart fatty acid binding protein.",
J. Biol. Chem. 262:9709-9717(1987).
                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                FILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVMKGVT 124
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                    64
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                                                                                                                                                                                                                                       5 FVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTEIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claffey K.P., Herrera V.L., Brecher P., Ruiz-Opazo N.; "Cloning and tissue distribution of rat heart fatty acid binding protein mRNA: identical forms in heart and skeletal muscle."; Blochemistry 26:7900-7904(1987).
                                                                                                                                                                                                                        ó,
                                                                                                                                                                                                    Length 131;
                                                                                                                                                                                                                      21; Indels
                                                                                                                                        E -> Q (IN REF. 3).
I -> T (IN REF. 3).
D -> N (IN REF. 3).
E53788F693BC6A0E CRC64;
                                                                                                                                                                                                ch 71.4%; Score 482; DB 1; Similarity 72.4%; Pred. No. 1.5e-36; 92; Conservative 14; Mismatches 21;
                                                                                               PROSITE; PS00214; FABF; 1.
MYelln; Lipid-binding; Transport; Acetylation.
0 0 1 ACETYLATION.
MOD_RES 1 1 ACETYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1988 (Rel. 07, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
FATTI ACID-BINDING PROTEIN, HEART (H-FABP).
or send an email to license@isb-sib.ch).
                                              HSSP; P02690; 1PMP.
InterPro: IPR000463; Fatty_acid_BP.
InterPro: IPR000566; Lipochl_cytFABP.
Pfam; PF00061; lipocalin; l.
PRINTS; PR00178; FATTYACIDBP.
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                     14791 MW;
                  EMBL; J03744; AAA31451.1; -. PIR; A03145; MPRB2. PIR; A28081; A28081.
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                                                                                                                                                                     131 AA;
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SEQUENCE FROM N.A.
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P07483;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
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MEDLINE-88326235; PubMed=3415652;
Jones P.D., Carne A., Bass N.M., Grigor M.R.;
"Isolation and characterization of fatty acid binding proteins from mammary tissue of lactating rats.";
Biochem. J. 251:919-925(1988).
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"Differentiational regulation and phosphorylation of the fatty acid-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Stomach:
MEDLINE-90032682; PubMed-2806260;
MEDLINE-90032682; PubMed-2806260;
Matsubara, Iseki S., Hitomi M., Kimura H., Odani S., Kondo H.,
Matsubara Y., Muto T., Ono T.;
"Purification and characterization of a fatty-acid-binding protein from the gastric mucosa of rats. Possible identity with heart fatty-acid-binding protein and its parietal cell localization.";
Eur. J. Biochem. 185:27-33(1989).
MEDLINE-86250713; PubMed=2424895; Sacchertini J.C., Said B., Schulz H., Gordon J.L.; Said B., Schulz H., Gordon J.L.; Rat heart fatty acid-binding protein is highly homologous to murine adipocyte 422 protein and the P2 protein of peripheral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-89374061; PubMed-2775193;
Kimura H., Hitomi M., Odani S., Koide T., Arakawa M., Ono T.;
"Rat heart fatty acid-binding protein. Evidence that supports amino acid sequence predicted from the CDNA.";
Biochem. J. 260:303-306(1989).
                                                                                                                                                                                                                                                                      TISSUE-Kidney;
MEDLINE-91170283; PubMed-2005132;
Kimura H., Odani S., Nishi S.-I., Sato H., Arakawa M., Onc
Primary structure and cellular distribution of two fatty
acid-binding proteins in adult rat kidneys.";
J. Biol. Chem. 266:5963-5972(1991).
                                                                                                                                                                        Biol. Chem. 261:8218-8223(1986)
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MEDLINE-94162301; PubMed-8117746;
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PIR; A39551; A39551.
PIR; S06478; S06478.
HSSP; P05413; 2HMB.
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PIR; A27452; A27452.
PIR; A28197; A28197.
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NCBI_TaxID=9606;
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INIT_MET
MOD_RES
MOD_RES
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P02689;
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MEDLINE-93054235; PubMed=1429365;
Binas B., Spitzer E., Zschlesche W., Erdmann B., Kurtz A., Mueller T.,
Niemann C., Blenau W., Grosse R.,
"Hormonal induction of functional differentiation and mammary-derived
growth inhibitor expression in cultured mouse mammary gland
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-ICR SWISS; TISSUE-Liver;
MEDLINE-95011621; PubMed-7926807;
Treunier M., Kozak C.A., Gallahan D., Grosse R., Mueller T.;
"Cloning and characterization of the mouse gene encoding mammary-derived growth inhibitor/heart-fatty acid-binding protein.";
Gene 147:237-242(1994).
                                                                                                                                                                                                  DAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTE 62
                                                                                                                                                                                                             2 DAFVGTWKLVDSKNFDDYMKSLGVGFATRQVASMTKPTTIIEKNGDTIIIKTHSTFKNTE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H-FABP.";
                                                                                                                                                                                                                                                                                                                                                                  P11404;
01-JUL-1999 (Rel. 11, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
FATIY ACID-BINDING PROTEIN, HEART (H-FABP) (MAMMARY-DERIVED GROWTH INHIBITOR) (MDGI).
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                PHOSPHORYLATION (BY TYR-KINASES).
S -> SN (IN REF. 3).
E -> Q (IN REF. 5).
F -> D (IN REF. 3).
731B4C66A8BFB45BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tweedle S., Edwards Y.; "cDNA sequence for mouse heart fatty acid binding protein, Nucleic Acids Res. 17:4374-4374(1989).
                                                                                                                                                        ;; Score 472; DB 1; Length 132;
;; Pred. No. 1.2e-35;
11; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (AUG-1989) to the EMBL/GenBank/DDBJ databases.
                                                Transport; Lipid-binding; Acetylation; Phosphorylation.
INIT_MET 0 0 0 MOD_RES 1 1 ACETYLATION.
                                                                                                                                                                                                                                                                                                                                                            132 AA.
InterPro; IPR000463; Fatty_acid_BP.
InterPro; IPR000566; Lipocln_cytFABP.
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MEDLINE-89296486; PubMed-2740224;
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        InterPro; IPR000566; Lipoclin_Pfam; PR0061; Lipocalin; I. PRNINS; PR00118; FATTACIDEP. PROSITE; PS00214; FABP; I.
                                                                                                                                                        69.9%;
70.5%;
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63
69
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14643 1
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Best Local Similarity 70.5%
Matches 91; Conservative
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                                                                                                                          132 AA;
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Tweedie S.;
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63
70
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ID FABH_MOUSE
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IN VILTO CELL. DEV. BIOL. 28A:625-634(1992).
-!- FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR TRANSPORT OF LONG-CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF TRANSPORTERS.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalía; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-92068191; Pubmed-1720307;
Hayasaka K., Nanao K., Tahara M., Sato W., Takada G., Miura M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACETYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY TYR-KINASES)
(BY SIMILARITY).
(BY GIN REF. 1).
D -> N (IN REF. 3 AND 4).
F78BAE6DACIABB6A CRC64;
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PRINTS; PR00178; FATTYACIDBP.
PROSITE; PS00214; FABP; 1.
Transport; Lipid-binding; Acetylation; Phosphorylation.
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69.0%; Pred. No. 4.1e-35;
ive 14; Mismatches 26;
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Last annotation update)
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EMBL, U02884; AAA61933.1; -.
EMBL, U02883; AAA03445.1; -.
PIR, S04591; S04591.
HSSP; P05413; 2HMB.
SWISS-2DPAGE; P11404; MOUSE.
MGD; MG195476; Fabp3.
InterPro; IPR000463; Fatty_acid_BP.
InterPro; IPR000566; Lipocin_cytFABP.
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01-MAY-1992 (Rel. 22, Last seq
20-AUG-2001 (Rel. 40, Last ann
MXELIN P2 PROTEIN.
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14689 MW;
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les 89; Conserv
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131 AA

'Isolation and sequence determination of cDNA encoding P2 protein of

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us-09-905-235-1.rsp

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X-RAI CRYSTALLOGRAPHY (2.7 ANGSTROMS).
MEDLINE-93253782; PubMed=7683727;
Gowan S.W., Mewcomer M.E., Jones T.A.;
"Crystallographic studies on a family of cellular lipophilic transport proteins. Refinement of P2 myelin protein and the structure determination and refinement of cellular retinol-binding protein in complex with all-trans-retinol.";
J. Mol. Biol. 230:1225-1246(1993).
-!- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN
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                                                                                                                                                                                                           Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                  Uyemura K.;
of the P2 protein in bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- FINILIATIY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF TRANSPORTERS.

PIR, A03144, MPBO2.

PDB; 1PMP; 26-JAN-95.

Interpro; IPR000463; Eatty_acid_BP
Interpro; IPR000566; Lipocaln_CytFRABP.

Pfam; PF00061; Lipocaln, 1.

PRINTS; PR00178; FATTYACIDBP.

PROSTE; PS00214; FABP, 1.

Myelin; Lipid-binding; Transport; Acetylation; 3D-structure.

MOD_RES.

1 ACETYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-89005045; PubMed-2458918;
Jones T.A., Bergfors T., Sedzik J., Unge T.;
"The three-dimensional structure of P2 myelin protein.";
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                                                                                                                 Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                Kitamura K., Suzuki M., Suzuki A., Uy
"The complete amino acid sequence of
peripheral nerve myelin.";
                                                           PRT;
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                                                                                                   Created)
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                                                             STANDARD;
                                                                                               21-JUL-1986 (Rel. 01,
21-JUL-1986 (Rel. 01,
20-AUG-2001 (Rel. 40,
MYELIN P2 PROTEIN.
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                                                                                                                                                                                             Bos taurus (Bovine).
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CTRIYEK 130
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                                                           MYP2_BOVIN
P02690;
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DISULFID
SEQUENCE
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                       RESULT 10
MYP2_BOVIN
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                                                                                                                                                                                                                                               "Partial structure and mapping of the human myelin P2 protein gene."; J. Neurochem. 63:2010-2013(1994).
-!- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 FKLGQBFEETTADNRKTKSIVTLQRGSLNQVQRWDGKETTIKRKLVNGKMVAECKMKGVV 123
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                                                                                             Uyemura K.;
human P2 protein.";
                                                                                                                                                                   SEQUENCE OF 1-115 FROM N.A.
MEDLINE-95054012; PubMed-7525873;
Narayanan V., Ripepi B., Jabs E.W., Hawkins A., Griffin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> GG (IN REF. 3).
-> N (IN REF. 2).
-> D (IN REF. 2).
3D0E640BA03E69D2 CRC64;
human peripheral myelin.";
Biochem. Biophys. Res. Commun. 181:204-207(1991)
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Myelin; Lipid-binding; Transport; Acetylation.
INIT_MET 0
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                                                                                           Suzuki M., Kitamura K., Sakamoto Y., "The complete amino acid sequence of J. Neurochem. 39:1759-1762(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000463; Fatty_acid_BP.
InterPro; IPR000566; Lipocln_cytFABP
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PRINTS; PR00178; FATTYACIDBP.
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MIM; 170715; -.
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Best Local Similarity
Matches 87; Conserv
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|124 CTRIYEK 130
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Marayanan V., Kaestner K.H., Tennekoon G.I.;
"Structure of the mouse myelin P2 protein gene.";
J. Neurochem. 57:75-80(1991).
-1- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN
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                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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01-MAR-1992 (Rel. 21, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MYELIN P2 PROTEIN.
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                                                                         STANDARD;
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                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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|124 CTRIYEK 130
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ID FABH_HUMAN
AC P05413; Q99957;
                                                                         MYP2_MOUSE
                                                                                            P24526
                                                     MYP2_MOUSE
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Wu X., Arit M., Goodfellow P.J., Rottman J.N.;
"Genomic organization and complete nucleotide sequence of the human cardiac fatty acid binding protein gene (FABP3), and identification of a closely related genomic sequence."; submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
01-NOV-1988 (Rel. 09, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
FATTY ACID-BINDING PROTEIN HEART (H-FABP) (MUSCLE FATTY ACID-BINDING
PROTEIN) (M-FABP) (MAMMARY-DERIVED GROWTH INHIBITOR) (MDGI).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-94085953; PubMed-8262516;
Troxler R.F., Offner G.D., Jiang J.W., Wu B.L., Skare J.C.,
Milunsky A., Wyandt H.E.;
"Localization of the gene for human heart fatty acid binding protein
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"Three-dimensional structure of recombinant human muscle fatty acid-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peeter R.A., Veerkamp J.H., Kanda T., Ono T., Geurts van Kessel A., "Cloning of the cDNA encoding human skeletal-muscle fatty-acid-binding protein, its peptide sequence and chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kovalyov L.I., Shishkin S.S., Efimochkin A.S., Kovalyova M.A., Ershova E.S., Egorov T.A., Musalyamov A.K.; "The major protein expression profile and two-dimensional protein database of human heart.";
                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Boerchers T., Hoejrup P., Nielsen S.U., Roepstorff P., Spener F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Knudsen J.; "Revision of the amino acid sequence of human heart fatty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hu Y.F., Ao X., Russo I.H., Russo J.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
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J. Biol. Chem. 267:18541-18550(1992).
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Mol. Cell. Biochem. 98:127-133(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Skeletal muscle;
MEDLINE-91248148; PubMed-1710107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-88339792; PubMed-3421901;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem. J. 276:203-207(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein from human'heart.";
Biochem. J. 252:191-198(1988).
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Hum. Genet. 92:563-566(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00214; FABP; 1.
Transport; Lipid-binding; Acetylation; Phosphorylation; 3D-structure.
INIT_MET 0 0 0 ACETYLATION.
MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES)
                PHOSPHORYLATION (BY TYR-KINASES) (BY SIMILARITY).
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InterPro; IPR000566; Lipocln_cytFABP.
Pfam; PF00061; lipocalin; 1.
  MEDLINE-95006319; PubMed-7922029;
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F; 08-MAY-95.
3; 31-JAN-94.
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JH0199; JH0199.
S15432; S15432.
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                                                                                                                                                                                                                                                                         63 ISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVMKG 122
                                                                                                                                                                                                                                                                                                                62 ISFKLGVEFDETTADDRKVKSIVTLDGGKLVHLQKWDGQETTLVRELIDGKLILTLTHGT 121
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                                                                           Gaps
                                                                                                                                        3 DAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTE 62
                                                                                                                                                                        2 DAFLGTWKLVDSKNFDDYMKSLGVGFATRQVASMTKPTTIIEKNGDILLLKTHSTFKNTE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cardiac fatty acid-binding proteins. Isolation and characterization of the mitochondrial fatty acid-binding protein and its structural relationship with the cytosolic isoforms."; J. Biol. Chem. 265:16255-16261(1990).
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01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
FATTY ACID-BINDING PROTEIN, HEART (H-FABP) (MAMMARY-DERIVED GROWTH INHIBITOR) (MDGI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
BIDLINE 8831264; PubMed=3409882;
Billich S., Wissel T., Kratzin H., Hahn U., Hagenhoff B.,
Lezius A.G., Spener F.;
"Cloning of a full-length complementary DNA for fatty-acid-binding protein from bovine heart.";
Eur. J. Biochem. 175:549-556(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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Unterberg C., Boerchers T., Hoejrup P., Roepstorff P., Knudsen J.,
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"Developmental regulation of mammary-derived growth inhibitor
expression in bothne mammary tissue.";
J. Cell Biol. 110:1779-1789(1990).
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       Length 132;
                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zabari M., Berri M., Rouchon P., Zamora F., Tassy C.,
Ribadeau-Dumas B., Ouali A.;
ch 65.9%; Score 445; DB 1;
1 Similarity 65.1%; Pred. No. 3.1e-33;
84; Conservative 16; Mismatches 29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 AA
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TISSUE-Mammary gland;
MEDLINE-90243786; PubMed-2335570;
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MEDLINE-94146156; PubMed-8312397;
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Query Match
Best Local Similarity
Matches 84; Conserv
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"Purification and characterisation of a polymorphic low M(r) bovine muscle cysteine proteinase inhibitor: structural identity with fatty-actio-binding proteins.";
Biochimie 75:937-945(1993).
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"Bound water in apo and holo bovine heart fatty-acid-binding protein
determined by heteronuclear NDR spectroscopy.";
Eur. J. Biochem. 251:781-786 (1998)

-!- FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR
TRANSPORT OF LONG-CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.
-!- FUNCTION: MOSI REVERSIBLY INHIBITS PROLIFERATION OF WAMMARY
CARCINOMA CELLS.
                                                                                                VARIANT IN POSITION 98.
MEDDINE-93358876; PubMed-8354262;
Bartetzko N., Lezius A.G., Spener F.;
"Isoforms of fatty-acid-binding protein in bovine heart are coded by distinct mRNA.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transport; Lipid-binding; Acetylation; Phosphorylation; 3D-structure
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                                                                                                                                                                                                                                                                                                    Saenger W.; "Three-dimensional structure of fatty-acid-binding protein from
                                                                                                                                                                                                                                                      MEDLINE-91301134, PubMed-2070787;
Mueller-Fahrnow A., Egner U., Jones T.A., Ruedel H., Spener F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARLIANGE CELLOS.

1. SUBCELLULAR LOCATION: CYTOPLASMIC OR MITOCHONDRIAL MATRIX.

1. TISSUE SPECIFICITY: MAMMARY EPITHELIAL CELLS OF DEVELOPING LOBULOALVEOLAR STRUCTURES AND HEART.

1. SIMILARIY: BELONGS TO THE FABP/P2/CRABP FAMILY OF TRANSPORTERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDB; IBWY: 07-CCT-98.
InterPro; IPR000463; Fatty_acid_BP.
InterPro; IPR000566; Lipocin_cytFABP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Blochem. 230:266-280(1995).
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MEDLINE-93130916; PubMed-1483473;
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MEDLINE=95324534; PubMed=7601110;
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MEDLINE=98149696; PubMed=9490052;
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PRINTS; PR00178; FATTYACIDBP.
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EMBL; X51933; CAA36199.1; -.
PIR; A29466; A29466.
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A37883; A37883.
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                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Suina; Suidae; Sus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-97262098; PubMed-9107676;
Gerbens F.N.A., Rettenberger G., Lenstra J.A., Veerkamp J.H.,
           ACETYLATION.
PHOSPHORYLATION (BY TYR-KINASES)
                                                                                                                                                         Length 132;
                                                                                                                                                                                  30; Indels
                                (BY SIMILARITY).

N -> D.

DSK -> SSE (IN REF. 4).

E -> S (IN REF. 4).

H -> Q (IN REF. 4).

T -> Q (IN REF. 4).

H -> Q (IN REF. 4).

H -> Q (IN REF. 4).

W; C6204932C6DFID35 CRC64;
                                                                                                                                                         Score 442; DB 1;
Pred. No. 5.7e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
FATTY ACID-BINDING PROTEIN, HEART (H-FABP).
                                                                                                                                                                                                                                                                                                                                                                                              132 AA
                                                                                                                                                                                  15; Mismatches
                                                                                                                                                           Score 442;
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InterPro; IPR000566; Lipocin_cytFABP.
Pfam: PF00061; lipocalin; 1.
PRIMTS; PR00178; FATTMACIDBP.
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                                                                                                                       14648 MW;
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                                                                                                                                                                                   84; Conservative
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93
 13
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Mammalia; Eutheria;
                                            98
12
40
43
93
127
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002772;
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                                                                                                                                                                        Schoentgen F., Pignede G., Bonanno L.M., Jolles P.;
"Fatty-acid-binding protein from bovine brain. Amino acid sequence and some properties.";
Eur. J. Biochem. 185:35-40(1989).
-!- FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR TRANSPORT OF LONG CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.
BINDS OLEIC AND PALMITIC ACIDS BUT NOT PALMITOYL COA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                          ACETYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY TYR-KINASES) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schoentgen F., Bonanno L.M., Pignede G., Jolles P.; "Amino acid sequence and some ligand binding properties of fatty acid-binding protein from bovine brain."; Mol. Cell. Biochem. 98:35-39(1990).
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                                                                                                     Ouery Match 65.5%; Score 442; DB 1; Length 132; Best Local Similarity 65.1%; Pred. No. 5.7e-33; Matches 84; Conservative 15; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBUNIT: MONOMER.
-1- SUBCELULAR LOCATION: CYTOPLASMIC.
-1- SIMILARIN: BELONGS TO THE FABF/P2/CRBF/CRABP FAMILY OF TRANSPORTERS.
  Acetylation; Phosphorylation. BY SIMILARITY.
                                                                B5431E65EF596C95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
FATTY ACID-BINDING PROTEIN, BRAIN (B-FABP).
                                                                                                                                                                                                                                                                                                                                                             131 AA.
                                                      SIMILARITY
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E -> D.
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InterPro; IPR000566; Lipocln_cytFABP.
Pfan; PF00061; lipocalin; 1.
PRINTS; PR00178; FATTACIDBP.
PROSITE; PS00214; FABP; 1.
Transport; Lipid-binding.
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MEDLINE-91094811; PubMed-2266968;
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15-JUL-1999 (Rel. 38, Last seq
15-JUL-1999 (Rel. 38, Last anno
                                                                 14618 MW;
Transport; Lipid-binding;
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MOD_RES 1 1 1
MOD_RES 19 19
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ID FABB_BOVIN
AC Q09139;
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                                                                                                                                                        Length 131;
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A26FF5D63C0CF2B4 CRC64;
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Pred. No. 1.9e-31;
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Best Local Similarity.
Matches 80; Conservi
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122 VVAVRHYEK 130
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January 24, 2002, 09:15:43; Search time 25.01 Seconds (without alignments) 772.009 Million cell updates/sec
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675
1 MCDAFVGTWKLVSSENFDDY.......KLVVECVMKGVTSTRVXERA 132
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_virus:*
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sp_unclassified:*

sp_phage:* sp_plant:* sp_rodent:*

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20 314 22 330 23 300 24 28 29 27 20 20 20 20 20 20 20 20 20 20	LT 1 60 099P60 PRELIMIN 099P60; 01-JUN-2001 (TrEMBLX SPERMOPHILUS tridece BUKARYOLE MELEZON; MARMMANIA; EUTHERIA; SPERMOPHILUS. NIBI_TAXID-43179;	SEQUENCE FROM N.A. Hittel D.S., Store File of the store o	1 MCDAFV MCDAFV
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PRINTS: PR00178; FATTACIDEP.
PROSITE; PS00214; FABP; 1.
SEQUENCE 134 AA: 14890 vm.
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(TrEMBLrel. 17, I
                                                                               Query Match
Best Local Similarity 94.7%;
Matches 107; Conservative
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Best Local Similarity 70.5%;
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                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shen W.-J., Sridhar K., Bernlohr D.A., Kraemer F.B.;
"Interaction of rat hormone-sensitive lipase with adipocyte lipid-binding protein.";
Proc. Natl. Acad. Sci. U.S.A. 96:5528-5532(1999).
EMBL; AF144756; AAD37371.1; --
HSSP; P04117; ILID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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STRAIN-NEW ZEALAND WHITE; TISSUE-BLADDER;
Guan Y., Zhang Y., Davis L., Breyer M.D.;
"Expression of aP2 gene in transitional epithelium of rabbit bladder.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 603; DB 11; Length 150;
Pred. No. 9.9e-46;
7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF136241; AAD32209.1; -.
HSSP; P04117; 1LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                         .00214; FABP; 1.
150 AA; 16468 MW; 9D214AB610D0C54E CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UNV-2001 (TrEMBLrel. 17, Last annotation update)
ADIPOCYTE LIPID-BINDING PROFEIN (FRAGMENT).
                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ADIPOCYTE LIPID-BINDING PROTEIN.
                                                                                                                                                                                                                                  STRAIN-SPRAGUE DAWLEY; TISSUE-ADIPOSE TISSUE;
MEDLINE-99254074; PubMed-10318917;
               150 AA
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Interpro; IPR000566; Lipocln_cytFABP.
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InterPro: IPR000566; Lipocln_cytFABP.
Pfam; PF00061; lipocalin; 1.
PRINTS; PR00178; FATTACIDBP.
PROSITE; PS00214; FABP; 1.
SEQUENCE 150 AA; 16468 MW; 9D214A
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                 PRT;
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                 PRELIMINARY;
                                                                                                                                   Rattus norvegicus (Rat).
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                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                  Q9R290;
               Q9R290
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SEQUENCE FROM N.A.
SERRALSTARY TISSUE-HEART;
PubMed-10561574;
Zhang J., Rickers-Haunerland J., Dawe I., Haunerland N.H.;
Zhang J., Rickers-Haunerland J., Dawe I., Haunerland N.H.;
"Structure and chromosomal location of the rat gene encoding the heart fatty acid-binding protein.";
Eur. J. Biochem. 266:347-321(1999).
EMBL; AF144090; AAF19003.1; -.
HSSP: P05413: HMT.
InterPro; IPR000466; Lipocln_cytFABP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID-10116;
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                                                                                                                                                                                                                                                     1 TWKLVSSENFDDTMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTEISFKL 60
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                                                                                                                                                                                                                          8 TWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTEISFIL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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                                                                                                                                                                                                                                                                                                                               68 GQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVM 120
                                                                                                                                                                                                                                                                                                                                                         Length 134;
                                                                                                                           Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.1%; Score 473.5; DB 11; Length 70.5%; Pred. No. 2.1e-34; Ive 12; Mismatches 26; Indels
                                                                                                                      Score 537; DB 6; Length 11 Pred. No. 4.4e-40; 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE87C12F10992FF4 CRC64;
1
113
12536 MW; 4C19A538EC897F4F CRC64;
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Last annotation update)
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Last sequence update)
Last annotation update)
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NCBI_TaxID=7955;
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                                                                                                            Q9XSI5;
                                                                                        Q9XSI5
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                                                                                                                                                                                       Hittel D.S., Storey K.B.;
"Differential expression of adipose- and heart-type fatty acid-binding proteins in hibernating ground squirrels.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF127854; AAK08083.1;
SEQUENCE 133 AA; 14853 MW; 9F3D6F6DB78AE721 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TEISFILGQEFÜEVTADDRKVKSTITLDGGVLVHVQKWDGKSTIIKRKREDDKLVVECVM 120
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spermophilus tridecemlineatus (Thirteen-lined ground squirrel).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
Sus.
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                                                                                                                                                                                                                                                                                                                                                                  Length 133;
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                                                                                                                                                                                                                                                                                                                                                                                                          28; Indels
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Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL: AF102872; AAC78684.1; --
HSSP: P04117; ILID.
                                                                                                                                                                                                                                                                                  . 9F3D6F6DB78AE721 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ADIPOCYTE FATTY ACID BINDING PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                           69.3%; Score 468; DB 11;
67.9%; Pred. No. 6.3e-34;
ive 14; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87 LDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVMKGVTS 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 AA.
HEART-TYPE FATTY ACID-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000463; Fatty_acid_BP.
InterPro; IPR000566; Lipocln_cytFABP.
Pfam; PF00061; lipocalin; 1.
PRINTS; PR00178; FATTYACIDBP.
                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 67.9%
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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Best Local Similarity
Matches 85; Conserv
                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                         NCBI_TaxID=43179;
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                                                                                                   Spermophilus
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SEQUENCE
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"Nucleotide sequence of cDNA clones coding for a brain-type fatty acid
binding protein and its tissue-specific expression in adult zebrafish
(Danio rerio).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 QEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVMKGVTSTRV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 WKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKNTEISFILG 68
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01-JUN-2001 (TIEMBLEEL. 17, Last annotation update)
BRAIN-TYPE FATTY-ACID BINNING PROTEIN.
Brachydanio reito (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cypriniformes; Cypriniformes; Danio.
                                                                                                                                                                               Eguus caballus (Horse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Eguus.
                                                                                                                                                                                                                                                                                                                                                                                   Schape F.G., Pelsers M.M.A.L., Van der Vusse G.J., Glatz J.F.C.;
"Cloning of equine H-FABP cDNA.";
submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF14350; AAD32219.1;
HSSP; P10790; 1BWY.
InterPro; IPR000463; Fatty_acid_BP.
InterPro; IPR000565; Lipocalin; 1.
Pfam; PF00061; lipocalin; 1.
PRINTS; PR00178; FATTYACIDBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.3%; Score 427; DB 6; Length 12
66.7%; Pred. No. 2.3e-30;
ive 13; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER 1 1
SEQUENCE 125 AA; 13965 MW; 9AF89C6A66B79D71 CRC64;
                                                                                    01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HEART-TYPE FATTY ACID-BINDING PROTEIN (FRAGMENT).
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EMBL. AR23712; AAF79948.1. .
InterPro: IPR000463; Fatty_actd_BP.
InterPro: IPR000566; Lipocin_cytFABP.
                                                           01-NOV-1999 (TrEMBLrel, 12, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 63.3%,
Best Local Similarity 66.7%,
Matches 82; Conservative
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PRELIMINARY;
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61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVM 120
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MEDLIND-98129752; Pubmed-9461533;
Vayda M.E., Londraville R.L., Cashon R.E., Costello L., Sidell B.D.;
"Two distinct types of fatty acid-binding protein are expressed in heart ventricle of Antarctic teleost fishes.";
Biochem. J. 330:375-382(1998).
EMBL; 092449; AAC6357.1; -...
                                                                 61 TEISFILGOEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Notothenloidei; Channichthyidae; Cryodraco.
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
  59.3%; Score 400; DB 13; Length 133; 58.3%; Pred. No. 6e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15011 MW; 1E691AA2738C75FF CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
FATTY ACID BINDING PROTEIN H8-ISOFORM.
                                                                                                                                                                                                                                                                                                                                                                01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) FATTY ACID BINDING PROTEIN H8-ISOFORM.
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InterPro; IPR000566; Lipocln_cytFABP.
                                                                                                                                                                                                                                                                                                                                                  Created)
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PRINTS; PR00178; FATTYACIDEP.
SEQUENCE 133 AA. 1501
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                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                            057668;
01-JUN-1998 (TrEMBLrel.
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121 DDVESIRRYVKA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cryodraco antarcticus
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                                                                                                                                                                                121 NNVVSTRIYER 131
                                                                                                                                                     121 KGVTSTRVYER 131
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Best Local Similarity
Matches 77; Conserv
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Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Arakawa K., Izawa M., Nishi K., Kiyosawa H., Rondo S., Yamanaka I.,
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Rasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Cosavant T.,
Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouakehoush J.,
Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner I., Washio T.,
Sakai K., Okido T., Furuno M., Anon H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Romstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. H.,
Lyons P., Marchlonni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Nymshay-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Nymschizaki V.
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                                                                                                                                Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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                                                                                     Length 132;
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                                                                                                                              Indels
PROSITE; PS00214; FABP; 1.
SEQUENCE 132 AA; 14918 MW; ED59506C71994C55 CRC64;
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Last annotation update)
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Pred. No. 3.9e-28;
                                                                                 61.2%; Score 413; DB 13;
llarity 59.1%; Pred. No. 4.3e-29;
Conservative 21; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.6%; Score 402; up 58.8%; Pred. No. 3.9e-tive 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 AA
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InterPro; IPR000463; Fatty_acid_BP.
InterPro; IPR000566; Lipocln_cytFABP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUE=TESTIS;
MEDLINE=21085660; Pubmed=11217851;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00214; FABP; SEQUENCE 132 AA; 1501
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121 EGVQAVRTYEKA 132
                                                                                                                                                                                                                                                                                                                                              121 KGVTSTRVYERA 132
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Best Local Similarity
Matches 77; Conservat
                                                                                   Query Match
Best Local Similarity
Matches 78; Conserv
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61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTIIKRKREDDKLVVECVM 120
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                                                                                                                                                                                                                                                                                                                                                                                              chaenocephalus aceratus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
Notothanioidei; Channichthyidae; Cryodraco.
NCBI_TaxID=36192, 36190;
                        1 MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN
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Last sequence update)
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Last annotation update)
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                                                                                                                                                                                                                                                                  134
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H8-FABP.
                                                                                                                                                                                                                                                                                                                                                  FATTY ACID BINDING PROTEIN H6-ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000463; Fatty_acid_BP.
InterPro; IPR000566; Lipocln_cytFABP
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                                                                                                                                                                                                                                                                                                                                                                                    Cryodraco antarcticus, and
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Matches 72; Conservative
                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                          121 KGVTSTRVYERA 132
                                                                                                                                                                   121 DDVESIRRYVKA 132
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01-JUN-1998 (
01-JUN-2001 (
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                                                                                TISSUE-HEART VENTRICLE;
MEDLINE-98129752; PubMed-9461533;
WEDLAGE, Londraville R.L., Cashon R.E., Costello L., Sidell B.D.;
"Two distinct types of farty acid-binding protein are expressed in heart ventricle of Antarctic teleost fishes.";
Blochen. J. 330:375-382(1998).
BRNBL; U94448; AG60356.1; --
HSSP; P10790; 1BWY.
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Biochem. J. 330:375-382(1998).
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ctinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
Notothenioidei; Nototheniidae; Gobionotothen.
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Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Notothenioidei; Channichthyidae; Chaenocephalus.
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                                                                                                                                                                                                                                                                                         133 AA; 15024 MW; 85157AA2665658C3 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                              58.8%; Score 397; DB 13; 57.6%; Pred. No. 1.1e-27;
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57.6%; Pred. No. 1.1e-27;
iive 19; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                              19; Mismatches
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01-JUN-1998 (TrEMBLrel. 06, Last seque
01-JUN-2001 (TrEMBLrel. 17, Last annot
FATTY ACID BINDING PROTEIN H8-ISOFORM.
                                                                                                                                                                                                                   InterPro; IPR000463; Fatty_acid_BP.
InterPro; IPR000566; Lipocln_cytFABP.
Pfam; PF00061; lipocalin; 1.
PRINTS; PR00178; FATTYACIDBP.
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InterPro; IPR000566; Lipocin_cytFABP
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TISSUE-HEART VENTRICLE;
MEDLINE-98129752; Pubmed-9461533;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00061; lipocalin; 1. PRINTS; PR00178; FATTYACIDBP
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 57.6%
Matches 76; Conservative
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Best Local Similarity 57.6
Matches 76; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 DDVESTRRYVKA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 AA;
                                 NCBI_TaxID-36190;
                                                                                                                                                                                                                                                                                            SEQUENCE
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H8-FABP

057670; 057670 RESULT 12 057670

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECVM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDVITIKSESTFKN 60
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Notothenioidei; Nototheniidae; Notothenia.
                                                                                                                             TISSUE-HEART VENTRICLE;
MEDLINE-98129752; PubMed-9461533;
Vayda M.E., Londraville R.L., Cashon R.E., Costello L., Sidell B.D.
Two distinct types of fatty acid-binding protein are expressed in heart ventricle of Antarctic teleost fishes.";
Blochem. J. 330:375-382(1998).
EMBL: U99450; AAC60358.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Biteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha Perciformes;
Notothenloidei, Bathydraconidae, Parachaenichthys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-HEART VENTRICLE;
MEDLINE-98129752; PubMed-9461533;
Wayda M.E., Londraville R.L., Cashon R.E., Costello L., Sidell B "Two distinct types of fatty acid-binding protein are expressed heart ventricle of Antarctic teleost fishes.";
Blochem. J. 330:375-382(1998).
BSD: U92447; AAC60355.1; --
HSSP: P10790; IBWY.
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                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 58.1%; Score 392; DB 13; Length 133; Best Local Similarity 56.8%; Pred. No. 3e-27; Matches 75; Conservative 19; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                        133 AA; 15008 MW; 851B94538D6E78DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D4CBCFC689121AFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
FATTY ACID BINDING PROTEIN H6-ISOFORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 AA
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Interpro: IPR000566; Lipocln_cytFABP.
Pfam; PF00061; lipocalin; 1.
PRINWS; PR00178; PATTAACIDBP.
                                                                                                                                                                                                                                                         HSSP, P10790; 1BWY.
InterPro; IPR000463; Fatty_acid_BP.
InterPro; IPR000565; Lipcoln_cytFABP.
Pfam; PF00061; lipccalin; 1.
PRINTS; PR00178; FATTYACIDBP.
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SEQUENCE 134 AA; 15161 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parachaenichthys charcoti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 KGVTSTRVYERA 132
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121 DDVESIRRYVKA 132
                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H6-FABP
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Length 134;

58.0%; Score 391.5; DB 13;

Query Match

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60 NTEISFILGQEFDEVTADDRKVKSTITLDGGVLVHVQKWDGKSTTIKRKREDDKLVVECV 119
                Gaps
                                               1 MCDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGD-VITIKSESTFK 59
                                                                   ; Pred. No. 3.4e-27; 23; Mismatches 34;
                                                                                                                                                                                                                                                                            Search completed: January 24, 2002, 09:18:54 Job time: 191 sec
 Best Local Similarity 55.49
Matches 72; Conservative
                                                                                                                                                                             120 MKGVTSTRVY 129
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                                                                               g
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